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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:52:05 ; Search time 35 Seconds
(without alignments)
597.724 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	811	99.9	157	19	AAW77077	Human interleukin
2	811	99.9	157	21	AAY57570	Human interleukin
3	811	99.9	157	22	AAE06661	Human interleukin-
4	811	99.9	157	22	AAG65294	Human interleukin-
5	811	99.9	157	22	AAG65351	Human interleukin-
6	811	99.9	157	23	ABB04389	Human IL-18. Homo
7	811	99.9	157	23	AAE16954	Human active inter
8	811	99.9	157	23	AAE17134	Human IL-18 protei
9	811	99.9	158	21	AAY85167	Human interleukin-
10	811	99.9	180	19	AAW48959	Wild-type human in
11	811	99.9	193	18	AAW22047	Interferon gamma i
12	811	99.9	193	19	AAW46592	Amino acid sequenc
13	811	99.9	193	22	AAB30541	A human IL-18 with
14	811	99.9	193	22	AAG63830	Amino acid sequenc
15	811	99.9	193	23	AAE16953	Human precursor in
16	811	99.9	233	23	AAE16959	Ubiquitin-human in
17	811	99.9	536	23	AAE16957	Human pro-IL-18/ca
18	811	99.9	588	23	AAE16958	Human pro-IL-18/ca
19	811	99.9	1048	23	AAE16960	Ubiquitin-human in
20	810	99.8	157	17	AAR99564	Human interferon-g
21	810	99.8	157	17	AAR99558	Human mature inter
22	810	99.8	157	18	AAW15701	Interferon-gamma i
23	810	99.8	157	18	AAW24258	Human protein for
24	810	99.8	157	19	AAW77158	Human interleukin-
25	810	99.8	157	19	AAW63810	Human IL-18 protei
26	810	99.8	157	19	AAW37741	IFN-gamma inducing
27	810	99.8	157	19	AAW52176	Interferon-gamma i
28	810	99.8	157	20	AAY39799	Interleukin-18 rec
29	810	99.8	157	21	AAY44597	Human interleukin-
30	810	99.8	157	21	AAY53904	Sequence of a matu
31	810	99.8	157	22	AAB82408	Human interleukin-
32	810	99.8	193	17	AAR99560	Human interferon-g
33	810	99.8	193	19	AAW37740	Interferon-gamma i
34	810	99.8	193	19	AAW52172	Interferon-gamma i
35	810	99.8	193	19	AAW47429	Interferon-gamma p
36	810	99.8	193	21	AAY53908	Amino acid sequenc
37	810	99.8	193	22	AAB82409	Human interleukin-
38	808	99.5	193	19	AAW77082	Interleukin 18 act
39	803	98.9	193	18	AAW31757	Interferon gamma i
40	801	98.6	157	19	AAW77083	Human interleukin
41	801	98.6	157	19	AAW48961	Mutant human inter
42	801	98.6	181	21	AAB23797	Human interleukin
43	792	97.5	193	22	AAY72608	Macaca cynomolgus
44	791	97.4	157	19	AAW77084	Human interleukin
45	791	97.4	157	19	AAW77085	Human interleukin

ALIGNMENTS

RESULT 1
AAW77077
ID AAW77077 standard; peptide; 157 AA.
XX
AC AAW77077;
XX
DT 16-NOV-1998 (first entry)
XX
DE Human interleukin 18.
XX
KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX
OS Homo sapiens.
XX
PN EP861663-A2.
XX
PD 02-SEP-1998.
XX
PF 24-FEB-1998; 98EP-0301352.
XX
PR 25-FEB-1997; 97JP-0055468.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX
DR WPI; 1998-448964/39.
DR N-PSDB; AAV48226.
XX
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,

PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
PT primary hyperthyroidism and osteoporosis
XX
PS Claim 4; Page 18; 56pp; English.
XX
CC Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157

RESULT 2
AAY57570
ID AAY57570 standard; protein; 157 AA.
XX
AC AAY57570;
XX
DT 06-MAR-2000 (first entry)
XX
DE Human interleukin 18 protein sequence SEQ ID NO:1.
XX
KW Human; interleukin 18; IL-18; potentiator; IGIF;tumour; cancer;
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
XX
OS Homo sapiens.
XX
PN WO9959565-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US11160.
XX
PR 21-MAY-1998; 98US-0086560.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Johnson RK;
XX
DR WPI; 2000-062368/05.
XX
PT New polypeptides, useful for preparation of composition for preventing
PT and/or treating cancer by inhibiting tumor growth
XX
PS Claim 1; Page 49-50; 53pp; English.
XX
CC The present sequence represents human interleukin 18 (IL-18). The
CC present invention describes a compound comprising human or murine IL-18
CC in combination with a chemotherapeutic agent (I). Also described are:
CC (1) a method of preventing and/or treating cancer in a mammal comprising
CC the administration of a cancer inhibiting amount of (I) comprising the
CC IL-18 protein and the chemotherapeutic agent and optionally a
CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
CC growth of tumour cells in a mammal sensitive to a composition comprising
CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
CC optionally a pharmaceutically acceptable carrier), comprising
CC administering to a mammal afflicted with the tumour cells an effective
CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
CC conjunction with a chemotherapeutic agent is useful in a method for
CC preventing and/or treating cancer in mammals by inhibiting the growth
CC of tumours or cancerous cells in mammals.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157

RESULT 3
AAE06661
ID AAE06661 standard; Protein; 157 AA.
XX
AC AAE06661;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human interleukin-1gamma (IL-1gamma) protein.
XX
KW Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Homo sapiens.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as

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CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present sequence is human
CC   interleukin-1gamma (IL-1gamma) protein related to the invention.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 22;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 4
AAG65294
ID   AAG65294 standard; protein; 157 AA.
XX
AC   AAG65294;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Human interleukin-18 (IL-18) protein fragment.
XX
KW   IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW   nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW   immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX
OS   Homo sapiens.
XX
PN   WO200158956-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04170.
XX
PR   10-FEB-2000; 2000US-0181608.
XX
PA   (BADI ) BASF AG.
XX
PI   Ghayur T,  Dixon RW,  Roguska M,  White M,  Labkovsky B,  Salfeld J;
PI   Duncan AR,  Brocklehurst SM,  Mankovich J,  Shorrock CP,  Thompson JE;
PI   Lennard SN;
XX
DR   WPI; 2001-550020/61.
XX
PT   Novel antibodies and compounds capable of binding to human
PT   interleukin-18 useful for treating, e.g., inflammatory disorders,
PT   neurological disorders, heart failure, myocardial infarction, and
PT   autoimmune diseases -
XX
PS   Disclosure; Page 9; 91pp; English.
XX
CC   The invention provides isolated antibodies, or antigen-binding portions,
CC   that are capable of binding to human interleukin-18 (IL-18). The
CC   antibodies may be used to inhibit human IL-18 activity in, and treat a
CC   disorder where IL-18 is detrimental in, a human subject suffering from,
CC   inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC   inflammatory bowel disease, and osteoarthritis), neurological disorders
CC   (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC   stroke), heart failure, myocardial infarction, autoimmune diseases such
CC   as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC   (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC   antibody may occur before, concurrent, or after administration of a
CC   second agent selected from an antibody, or fragment, capable of binding
CC   human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC   cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC   agents. The present sequence represents a human IL-18 protein fragment.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 22;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
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Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db      61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 5
AAG65351
ID   AAG65351 standard; protein; 157 AA.
XX
AC   AAG65351;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Human interleukin-18 (IL-18) protein fragment.
XX
KW   IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW   nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW   immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX
OS   Homo sapiens.
XX
PN   WO200158956-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04170.
XX
PR   10-FEB-2000; 2000US-0181608.
XX
PA   (BADI ) BASF AG.
XX
PI   Ghayur T,  Dixon RW,  Roguska M,  White M,  Labkovsky B,  Salfeld J;
PI   Duncan AR,  Brocklehurst SM,  Mankovich J,  Shorrock CP,  Thompson JE;
PI   Lennard SN;
XX
DR   WPI; 2001-550020/61.
XX
PT   Novel antibodies and compounds capable of binding to human
PT   interleukin-18 useful for treating, e.g., inflammatory disorders,
PT   neurological disorders, heart failure, myocardial infarction, and
PT   autoimmune diseases -
XX
PS   Disclosure; Page 14; 91pp; English.
XX
CC   The invention provides isolated antibodies, or antigen-binding portions,
CC   that are capable of binding to human interleukin-18 (IL-18). The
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CC   antibodies may be used to inhibit human IL-18 activity in, and treat a
CC   disorder where IL-18 is detrimental in, a human subject suffering from,
CC   inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC   inflammatory bowel disease, and osteoarthritis), neurological disorders
CC   (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC   stroke), heart failure, myocardial infarction, autoimmune diseases such
CC   as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC   (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC   antibody may occur before, concurrent, or after administration of a
CC   second agent selected from an antibody, or fragment, capable of binding
CC   human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC   cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC   agents. The present sequence represents a human IL-18 protein fragment.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 22;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 6
ABB04389
ID   ABB04389 standard; protein; 157 AA.
XX
AC   ABB04389;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Human IL-18.
XX
KW   Human; IL-18; interleukin-18; cancer.
XX
OS   Homo sapiens.
XX
PN   CN1326992-A.
XX
PD   19-DEC-2001.
XX
PF   07-JUN-2000; 2000CN-0107993.
XX
PR   07-JUN-2000; 2000CN-0107993.
XX
PA   (SHUA-) SHUANGLU PHARM CO LTD BEIJING.
XX
PI   Xu M,  Wang Y,  Huang X;
XX
DR   WPI; 2002-217571/28.
DR   N-PSDB; ABL41315.
XX
PT   Gene cloning, product preparation and use of Chinese interleukin-18
PT   subtype (53 Arg IL-18), useful for treating of cancer and other disease
PT   -
XX
PS   Claim 1; Page 7 (Disclosure); 8pp; Chinese.
XX
CC   The invention relates to the preparation of recombinant human
CC   interleukin-18 for treating of cancer and other disease.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 23;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
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Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 7
AAE16954
ID   AAE16954 standard; Protein; 157 AA.
XX
AC   AAE16954;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human active interleukin-18 (IL-18) protein.
XX
KW   Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;
KW   immunocompetent.
XX
OS   Homo sapiens.
XX
PN   WO200198455-A2.
XX
PD   27-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US18804.
XX
PR   15-JUN-2000; 2000US-211832P.
PR   10-AUG-2000; 2000US-224128P.
PR   20-JAN-2001; 2001US-264923P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Johanson KO,  Kirkpatrick RB,  Shatzman AR,  Ho YS,  Mcdevitt P;
XX
DR   WPI; 2002-139786/18.
XX
PT   Activation of precursor polypeptide e.g. interleukin-18 polypeptide
PT   useful for inducing interferon-gamma production,  comprises contacting
PT   or co-expressing caspase 4 or caspase 5 with precursor polypeptide  -
XX
PS   Claim 9; Fig 3; 64pp; English.
XX
CC   The invention relates to a method for the in vitro activation of human
CC   precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
CC   method comprises contacting precursor IL-18 with an activating enzyme
CC   such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
CC   of cysteine proteases that include interleukin-1beta converting enzyme
CC   (ICE), which preferentially cleave substrates containing a protease
CC   activation motif.The methods are useful for producing physiologically
CC   active polypeptide e.g. active IL-18 polypeptide. The active IL-18
CC   polypeptide has an activity of inducing the production of interferon
CC   (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
CC   biologically active substance for stimulating the production of IFNg
CC   from KG-1 (human myelomonocytic cell line) cells. The present sequence
CC   is human active IL-18 protein.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 23;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 8
AAE17134
ID   AAE17134 standard; Protein; 157 AA.
XX
AC   AAE17134;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human IL-18 protein.
XX
KW   Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;
KW   influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;
KW   hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;
KW   HPV; hepatitis C virus; HCV.
XX
OS   Homo sapiens.
XX
PN   WO200193898-A1.
XX
PD   13-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-US17924.
XX
PR   02-JUN-2000; 2000US-208869P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Esser KM,  Rosenberg M,  Tal-Singer R,  Woodnutt G,  Chisari FV;
XX
DR   WPI; 2002-154554/20.
XX
PT   Treatment of disease caused by e.g. influenza virus comprises
PT   administration of composition containing polypeptide, having identity
PT   of amino acid sequences  -
XX
PS   Claim 1; Fig 1; 41pp; English.
XX
CC   The invention relates to a method for treating viral diseases with
CC   IL-18, also known as interferon-gamma-inducing factor (IGIF) and IL-18
CC   combinations. The method involves administering a composition
CC   comprising IL-18 and IL-18 in combination with other agents. The method
CC   is used for treating diseases caused by viruses such as influenza virus,
CC   human immunodeficiency virus (HIV), herpes simplex virus (HSV),
CC   hepatitis A virus (HAV), hepatitis B virus (HBV), human papillomavirus
CC   (HPV) and hepatitis C virus (HCV). The present sequence is human
CC   IL-18 protein.
XX
SQ   Sequence   157 AA;

  Query Match             99.9%;  Score 811;  DB 23;  Length 157;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 9
AAY85167
ID   AAY85167 standard; Protein; 158 AA.
XX
AC   AAY85167;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Human interleukin-18 (IL-18) amino acid sequence.
XX
KW   Interleukin-18; production; IL-18; human; medical injection product.
XX
OS   Homo sapiens.
XX
PN   CN1243130-A.
XX
PD   02-FEB-2000.
XX
PF   24-JUL-1998;   98CN-0103307.
XX
PR   24-JUL-1998;   98CN-0103307.
XX
PA   (WUGG/) WU G.
XX
PI   Wu G,  Liu Z;
XX
DR   WPI; 2000-340020/30.
DR   N-PSDB; AAA10526.
XX
PT   Preparation method for engineering bacteria for recombination of human
PT   interleukin-18 and its product thereof -
XX
PS   Claim 1; Page 2; 17pp; English.
XX
CC   This sequence represents the human interleukin-18 (IL-18) amino acid
CC   sequence. The invention relates to a method for engineering bacterium for
CC   recombination of human IL-18 and a method for the preparation of IL-18. A
CC   primer containing a restriction endonuclease site can be used to
CC   accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
CC   stop codon preferred by coli bacillus to raise the expression rate. The
CC   method uses a  high-amplification culture medium to increase the
CC   expression level and only requires a one-step purification process to
CC   obtain a medical injection-pure product.
XX
SQ   Sequence   158 AA;

  Query Match             99.9%;  Score 811;  DB 21;  Length 158;
  Best Local Similarity   99.4%;  Pred. No. 7.2e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 61

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 121

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 158


RESULT 10
AAW48959
ID   AAW48959 standard; Peptide; 180 AA.
```

```
XX
AC   AAW48959;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Wild-type human interferon-gamma inducing factor.
XX
KW   Interferon-gamma inducing factor; interferon-gamma; killer cell;
KW   antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW   hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW   osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /note= "Signal peptide"
FT   Protein         24..180
FT                   /note= "Mature human IGIF which is claimed by the
FT                          inventors under claim 3 in the specification"
XX
PN   EP845530-A2.
XX
PD   03-JUN-1998.
XX
PF   28-NOV-1997;   97EP-0309632.
XX
PR   14-NOV-1997;   97JP-0329715.
PR   29-NOV-1996;   96JP-0333037.
PR   21-JAN-1997;   97JP-0020906.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Kurimoto M,  Okamoto I,  Yamamoto K;
XX
DR   WPI; 1998-288747/26.
DR   N-PSDB; AAV32754.
XX
PT   Mutants of interferon-gamma inducing polypeptide - useful as
PT   antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX
PS   Claim 3; pages 36-37; 59pp; English.
XX
CC   The present sequence represents the wild-type human interferon-gamma
CC   inducing factor (IGIF).  The invention provides for mutant human and
CC   mouse interferon-gamma inducing factors in which one or more cysteine
CC   residues are replaced with different residues at or away from the
CC   consensus sequences shown in AAW48956-W48958.  The mutant IGIFs are
CC   capable of stimulating immunocompetent cells for the production of
CC   interferon-gamma and are claimed to be less toxic, more active and
CC   stable than the corresponding wild type IGIF.  The mutant IGIFs are also
CC   claimed to enhance killer cell cytotoxicity and/or induce killer cell
CC   formation, and may therefore be useful as antitumour agents, antitumour
CC   immunotherapeutics, antiviral agents and antimicrobial agents.  The
CC   mutant IGIFs are also claimed to be useful for treating hepatitis,
CC   acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
CC   malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
CC   thrombopenia caused by radiation-  and chemo-therapy.
XX
SQ   Sequence   180 AA;

  Query Match             99.9%;  Score 811;  DB 19;  Length 180;
  Best Local Similarity   99.4%;  Pred. No. 8.6e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 83

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 143

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     144 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 180


RESULT 11
AAW22047
ID   AAW22047 standard; Protein; 193 AA.
XX
AC   AAW22047;
XX
DT   14-JAN-1998  (first entry)
XX
DE   Interferon gamma inducing factor-2 (IGIF-2) protein.
XX
KW   Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
KW   inflammation; proliferation; differentiation; maturation; tissue damage;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO9724441-A1.
XX
PD   10-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US20432.
XX
PR   29-DEC-1995;   95US-0580667.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Cocks BG,  Coleman R,  Hawkins PR;
XX
DR   WPI; 1997-363677/33.
DR   N-PSDB; AAT74987.
XX
PT   Novel interferon gamma inducing factor-2 - used to screen for
PT   compounds to diagnose, treat or prevent tissue damage associated
PT   with inflammation
XX
PS   Claim 1; Page 46; 60pp; English.
XX
CC   This is the protein sequence of interferon gamma inducing factor-2
CC   (IGIF-2). An IGIF-2 variant (AAW31757) and an IGIF variant (AAW22049),
CC   which may be an alternate transcript, also exist. Probes derived from
CC   the nucleic acid sequences can be used to quantify the expression of
CC   IGIF-2 in conditions that are associated with inflammation or aberrant
CC   expression of IGIF-2. The protein can be used to screen for compounds
CC   that interact with IGIF-2, such as antibodies, antagonists or other
CC   inhibitors (especially ribozymes or antisense sequences) of IGIF-2
CC   expression or activity. The protein can also be used to diagnose,
CC   prevent or treat IGIF-2 induction of proliferation, differentiation or
CC   maturation of leucocytes or lymphocytes, especially in relation to tissue
CC   damage associated with inflammation.
XX
SQ   Sequence   193 AA;

  Query Match             99.9%;  Score 811;  DB 18;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193
```

```
RESULT 12
AAW46592
ID   AAW46592 standard; Protein; 193 AA.
XX
AC   AAW46592;
XX
DT   21-MAY-1998  (first entry)
XX
DE   Amino acid sequence of human interleukin-1-gamma.
XX
KW   Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
KW   induction; antibody; diagnostic assay; fusion protein; activity;
KW   immunological disorder; allergy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          41..47
FT                   /note= "beta-1 region"
FT   Region          55..59
FT                   /note= "beta-2 region"
FT   Region          64..68
FT                   /note= "beta-3 region"
FT   Region          83..88
FT                   /note= "beta-4 region"
FT   Region          96..102
FT                   /note= "beta-5 region"
FT   Region          108..113
FT                   /note= "beta-6 region"
FT   Region          115..120
FT                   /note= "beta-7 region"
FT   Region          137..143
FT                   /note= "beta-8 region"
FT   Region          147..153
FT                   /note= "beta-9 region"
FT   Region          160..164
FT                   /note= "beta-10 region"
FT   Region          170..175
FT                   /note= "beta-11 region"
FT   Region          187..191
FT                   /note= "beta-12 region"
XX
PN   WO9744468-A1.
XX
PD   27-NOV-1997.
XX
PF   16-MAY-1997;   97WO-US07282.
XX
PR   20-MAY-1996;   96US-0651998.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hardiman GT,  Kastelein RA,  Sana TR,  Timans JC;
XX
DR   WPI; 1998-018522/02.
DR   N-PSDB; AAV05368.
XX
PT   Antagonist of human interleukin-1-gamma - used for treating
PT   immunological disorders caused by human IL-1-gamma
XX
PS   Disclosure; Pages 54-55; 63pp; English.
XX
CC   The present sequence represents human interleukin-1-gamma (IL-1-gamma).
CC   The protein is the human equivalent of a mouse cytokine, IGIF, which
CC   induces certain T cells to produce interferon-gamma. Human IL-1-gamma
CC   and mouse IGIF show 71% identity at the nucleotide level and
CC   approximately 65% identity at the amino acid level. Antagonists of
CC   IL-1 gamma, e.g. antibodies, can be used in a method for treating a
CC   condition caused by human IL-1 gamma. The antibodies can also be used
CC   in diagnostic assays. The IL-1-gamma protein can be covalently
CC   conjugated to polyethylene glycol or to a polypeptide, and the fusion
CC   protein used in a pharmaceutical composition for supplying the
CC   biological activity of IL-1 gamma. Conditions that can be treated using
CC   the human IL-1-gamma protein include immunological disorders, allergies,
CC   and infectious diseases. The IL-1-gamma can also be used to detect the
CC   presence of the protein or its receptor.
XX
SQ   Sequence   193 AA;

  Query Match             99.9%;  Score 811;  DB 19;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 13
AAB30541
ID   AAB30541 standard; Protein; 193 AA.
XX
AC   AAB30541;
XX
DT   06-MAR-2001  (first entry)
XX
DE   A human IL-18 with a caspase-8 cleavage site.
XX
KW   Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   33..36
FT                   /note= "caspase-8 cleavage site"
XX
PN   WO200061768-A2.
XX
PD   19-OCT-2000.
XX
PF   13-APR-2000; 2000WO-IL00220.
XX
PR   13-APR-1999;   99IL-0129427.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Rubinstein M,  Liu B,  Novick D,  Dinarello C,  Graber P;
XX
DR   WPI; 2001-006910/01.
DR   N-PSDB; AAC62200.
XX
PT   Preparation of biologically active molecules from its inactive
PT   precursors, comprises mutating their native cleavage site to a site
PT   capable of being cleaved by protease and cleaving the mutated molecule
PT   -
XX
PS   Disclosure; Fig 8a-b; 40pp; English.
XX
CC   The present sequence represents a human pro interleukin-18 (IL-18)
CC   with a caspase-8 cleavage site. The natural cleavage site of Il-18
CC   was mutated to a site susceptible to cleavage by a common protease.
CC   The specification describes a method for the preparation of biologically
CC   active molecules from their biologically inactive precursors. The method
CC   comprises mutating the native cleavage site to a site capable of being
CC   cleaved by a protease and cleaving the mutated molecule to yield the
CC   active compound. The method is especially used to produce active
```

```
CC   cytokines, such as IL-18.
XX
SQ   Sequence   193 AA;

  Query Match             99.9%;  Score 811;  DB 22;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 14
AAG63830
ID   AAG63830 standard; Protein; 193 AA.
XX
AC   AAG63830;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Amino acid sequence of human interleukin 18 (IL-18).
XX
KW   T-cell-helper type 2 response; Th2 response; T cell mediated response;
KW   allergic response; interleukin 18; IL-18; IgE-mediated allergy;
KW   allergic asthma; anaphylactic reaction; asthma associated allergy;
KW   IgE dependent allergic rhinoconjunctivitis.
XX
OS   Homo sapiens.
XX
PN   WO200168896-A1.
XX
PD   20-SEP-2001.
XX
PF   02-MAR-2001; 2001WO-US06869.
XX
PR   10-MAR-2000; 2000US-0188311.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Levy S,  Dekruyff RH,  Umetsu DT,  Maecker H;
XX
DR   WPI; 2001-570874/64.
DR   N-PSDB; AAH78060.
XX
PT   Reducing antigen specific immune response in conditions such as asthma,
PT   allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
PT   antigen-specific allergic response -
XX
PS   Disclosure; Page 36; 38pp; English.
XX
CC   The specification describes a method for reducing a T-cell-helper
CC   type 2 (Th2) T cell mediated antigen-specific allergic response. The
CC   method comprises administering a DNA construct encoding a fusion
CC   protein of interleukin 18 (IL-18) and an antigen associated with the
CC   allergic response. The method is useful for reducing a Th2 T cell
CC   mediated antigen-specific allergic response especially IgE-mediated
CC   allergic asthma or anaphylactic reactions or IgE dependent allergic
CC   rhinoconjunctivitis, and for treating asthma associated allergies where
CC   the allergies are ongoing at the time of the administration. The
CC   present sequence represents a human IL-18, and is used to construct
CC   fusion proteins of the invention.
XX
SQ   Sequence   193 AA;

  Query Match             99.9%;  Score 811;  DB 22;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-83;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 15
AAE16953
ID   AAE16953 standard; Protein; 193 AA.
XX
AC   AAE16953;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human precursor interleukin-18 (Pro-IL-18) protein.
XX
KW   Human; precursor interleukin-18; pro-IL-18; caspase; interferon gamma;
KW   IFN-gamma; immunocompetent.
XX
OS   Homo sapiens.
XX
PN   WO200198455-A2.
XX
PD   27-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US18804.
XX
PR   15-JUN-2000; 2000US-211832P.
PR   10-AUG-2000; 2000US-224128P.
PR   20-JAN-2001; 2001US-264923P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Johanson KO,  Kirkpatrick RB,  Shatzman AR,  Ho YS,  Mcdevitt P;
XX
DR   WPI; 2002-139786/18.
DR   N-PSDB; AAD27364.
XX
PT   Activation of precursor polypeptide e.g. interleukin-18 polypeptide
PT   useful for inducing interferon-gamma production,  comprises contacting
PT   or co-expressing caspase 4 or caspase 5 with precursor polypeptide  -
XX
PS   Claim 7; Fig 1; 64pp; English.
XX
CC   The invention relates to a method for the in vitro activation of human
CC   precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
CC   method comprises contacting precursor IL-18 with an activating enzyme
CC   such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
CC   of cysteine proteases that include interleukin-1beta converting enzyme
CC   (ICE), which preferentially cleave substrates containing a protease
CC   activation motif.The methods are useful for producing physiologically
CC   active polypeptide e.g. active IL-18 polypeptide. The active IL-18
CC   polypeptide has an activity of inducing the production of interferon
CC   (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
CC   biologically active substance for stimulating the production of IFNg
CC   from KG-1 (human myelomonocytic cell line) cells. The present sequence
CC   is human Pro-IL-18 protein.
XX
SQ   Sequence   193 AA;

  Query Match             99.9%;  Score 811;  DB 23;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-83;
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Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193
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Search completed: April 4, 2003, 10:59:30
Job time : 36 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:59:00 ; Search time 14 Seconds
(without alignments)
329.957 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	810	99.8	157	2	US-08-896-605A-6	Sequence 6, Appli
2	810	99.8	157	2	US-08-896-501A-4	Sequence 4, Appli
3	810	99.8	157	3	US-08-884-324-1	Sequence 1, Appli
4	810	99.8	157	3	US-08-996-338-26	Sequence 26, Appl
5	810	99.8	157	4	US-08-558-818-1	Sequence 1, Appli
6	810	99.8	157	4	US-08-974-469A-1	Sequence 1, Appli
7	810	99.8	157	4	US-08-832-180-1	Sequence 1, Appli
8	810	99.8	157	4	US-08-832-198-6	Sequence 6, Appli
9	810	99.8	157	4	US-09-819-902-6	Sequence 6, Appli
10	810	99.8	157	4	US-09-752-510-6	Sequence 6, Appli
11	810	99.8	193	2	US-08-896-605A-2	Sequence 2, Appli
12	810	99.8	193	2	US-08-896-501A-2	Sequence 2, Appli
13	810	99.8	193	4	US-08-832-180-9	Sequence 9, Appli
14	792	97.5	193	4	US-09-597-576-2	Sequence 2, Appli
15	513	63.2	157	2	US-08-502-535B-2	Sequence 2, Appli
16	513	63.2	157	2	US-08-908-005A-2	Sequence 2, Appli
17	513	63.2	157	3	US-08-996-338-27	Sequence 27, Appl
18	513	63.2	157	4	US-08-558-818-7	Sequence 7, Appli
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20	513	63.2	157	4	US-08-832-180-8	Sequence 8, Appli
21	513	63.2	157	4	US-08-832-198-11	Sequence 11, Appl
22	513	63.2	157	4	US-09-253-523-2	Sequence 2, Appli
23	513	63.2	157	4	US-09-251-911-2	Sequence 2, Appli
24	513	63.2	157	4	US-09-819-902-11	Sequence 11, Appl
25	513	63.2	157	4	US-09-752-510-11	Sequence 11, Appl
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27	259	31.9	50	4	US-09-819-902-2	Sequence 2, Appli
28	259	31.9	50	4	US-09-752-510-2	Sequence 2, Appli
29	96	11.8	25	4	US-08-558-818-4	Sequence 4, Appli
30	96	11.8	25	4	US-08-974-469A-4	Sequence 4, Appli
31	96	11.8	25	4	US-08-832-180-4	Sequence 4, Appli
32	96	11.8	25	4	US-08-832-198-8	Sequence 8, Appli
33	96	11.8	25	4	US-09-819-902-8	Sequence 8, Appli
34	96	11.8	25	4	US-09-752-510-8	Sequence 8, Appli
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36	90	11.1	17	4	US-09-819-902-5	Sequence 5, Appli
37	90	11.1	17	4	US-09-752-510-5	Sequence 5, Appli
38	81	10.0	155	6	5494663-8	Patent No. 5494663
39	81	10.0	267	6	5494663-5	Patent No. 5494663
40	76.5	9.4	270	2	US-08-611-880-1	Sequence 1, Appli
41	76.5	9.4	270	4	US-09-085-305-13	Sequence 13, Appl
42	75.5	9.3	270	4	US-09-085-305-20	Sequence 20, Appl
43	75	9.2	267	4	US-09-134-001C-3520	Sequence 3520, Ap
44	73	9.0	270	4	US-09-085-305-14	Sequence 14, Appl
45	72.5	8.9	268	4	US-09-085-305-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-605A-6

Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
;  GENERAL INFORMATION:
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  PROCESS FOR PRODUCING POLYPEPTIDE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/896,501A
;      FILING DATE:  18-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 213,267/1996
;      FILING DATE:  25-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 31,474/1997
;      FILING DATE:  31-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  TANIMOTO=3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-896-501A-4

  Query Match             99.8%;  Score 810;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

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Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
;  GENERAL INFORMATION:
;    APPLICANT:  Takanori OKURA
;    APPLICANT:  Kakuji TORIGOE
;    APPLICANT:  Masahi KURIMOTO
;    TITLE OF INVENTION:  GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
;    TITLE OF INVENTION:  OF INDUCING THE PRODUCTION OF INTERFERON-
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/884,324
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 185,305/96
;      FILING DATE:  27-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  OKURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-884-324-1

  Query Match             99.8%;  Score 810;  DB 3;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
;  GENERAL INFORMATION:
;    APPLICANT:  TORIGOE, Kakuji
;    APPLICANT:  OKURA, Takanori
;    APPLICANT:  KURIMOTO, Musashi
```

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;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/996,338
;      FILING DATE:  22-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 74,697/1997
;      FILING DATE:  12-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 215,488/1997
;      FILING DATE:  28-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 291,837/1997
;      FILING DATE:  09-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  TORIGOE-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-996-338-26

  Query Match             99.8%;  Score 810;  DB 3;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
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Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

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Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 5
US-08-558-818-1
; Sequence 1, Application US/08558818
; Patent No. 6197297
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:  NAME:KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
;    APPLICANT:  KENKYUJO
;    APPLICANT:  KUNIKATA, Toshio
;    APPLICANT:  TANIGUCHI, Mutsuko
;    APPLICANT:  KOHNO, Keizo
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
;    TITLE OF INVENTION:  WHICH INDUCES INTERFERON-  PRODUCTION
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect Version 5.0
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  FELICI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/558,818
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  JP 58,240/95
;    PRIOR APPLICATION DATA:  February 23, 1995
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-558-818-1

  Query Match             99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
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Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 6
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
;  GENERAL INFORMATION:
;    APPLICANT:  KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
;    APPLICANT:  KENKYUJO
;    APPLICANT:  TORIGOE, Kakuji
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  FUKUDA, Shigeharu
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  AGENT FOR SUSCEPTIVE DISEASE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect Version 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,469A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,879
;      FILING DATE:
;      APPLICATION NUMBER:  JP 78,357/95
;      FILING DATE:  March 10, 1995
;      APPLICATION NUMBER:  JP 274,988/95
;      FILING DATE:  September 29, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  TORIGOE=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-974-469A-1

  Query Match             99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 7
US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
;  GENERAL INFORMATION:
;    APPLICANT:  KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
;    APPLICANT:  KENKYUJO
;    APPLICANT:  USHIO, Shimpei
;    APPLICANT:  TORIGOE, Kakuji
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  OKAMURA, Haruki
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  INTERFERON-  PRODUCTION INDUCING
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect Version 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,180
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/558,191
;      FILING DATE:
;      APPLICATION NUMBER:  JP 304,203/94
;      FILING DATE:  No. 6214584ember 15, 1994
;      APPLICATION NUMBER:  10048102
;      FILING DATE:  September 18, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  USHIO=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-832-180-1

  Query Match             99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 8
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
;  GENERAL INFORMATION:
;    APPLICANT:  AKITA, Kenji
;    APPLICANT:  NUKADA, Yoshiyuki
;    APPLICANT:  FUJII, Mitsukiyo
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;    TITLE OF INVENTION:  PRODUCTION BY IMMUNOCOMPETENT CELL
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK, P.L.L.C.
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,198
;      FILING DATE:  08-APR-1997
;      CLASSIFICATION:  514
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/721,018
;      FILING DATE:  25-SEP-1996
;      APPLICATION NUMBER:  JP 95-270725
;      FILING DATE:  26-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 96-067434
;      FILING DATE:  29-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP not yet received
;      FILING DATE:  20-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  AKITA-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  "Xaa" in position 73 is either
;      OTHER INFORMATION:  'Ile' or 'Thr'
US-08-832-198-6

  Query Match             99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 9
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
;   GENERAL INFORMATION:
;        APPLICANT: AKITA, Kenji
;                   NUKADA, Yoshiyuki
;                   FUJII, Mitsukiyo
;                   TANIMOTO, Tadao
;                   KURIMOTO, Masashi
;        TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;                            PRODUCTION BY IMMUNOCOMPETENT CELL
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;             STREET: 419 Seventh Street N.W., Ste. 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/819,902
;             FILING DATE: 29-Mar-2001
;             CLASSIFICATION: 514
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/832,798
;             FILING DATE: 25-SEP-1996
;             APPLICATION NUMBER: JP 95-270725
;             FILING DATE: 26-SEP-1995
;             APPLICATION NUMBER: JP 96-067434
;             FILING DATE: 29-FEB-1996
;             APPLICATION NUMBER: JP not yet received
;             FILING DATE: 20-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: AKITA-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 628-5197
;             TELEFAX: (202) 737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 157 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FEATURE:
;             OTHER INFORMATION:  "Xaa" in position 73 is either
;             'Ile' or 'Thr'
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-819-902-6

  Query Match             99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 10
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
;   GENERAL INFORMATION:
;        APPLICANT: AKITA, Kenji
;                   NUKADA, Yoshiyuki
;                   FUJII, Mitsukiyo
;                   TANIMOTO, Tadao
;                   KURIMOTO, Masashi
;        TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;                            PRODUCTION BY IMMUNOCOMPETENT CELL
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;             STREET: 419 Seventh Street N.W., Ste. 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
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;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/752,510
;            FILING DATE: 03-Jan-2001
;          PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/721,018
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 96-067434
;            FILING DATE: 29-FEB-1996
;            APPLICATION NUMBER: JP not yet received
;            FILING DATE: 20-SEP-1996
;          ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: AKITA=1
;          TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 628-5197
;            TELEFAX: (202) 737-3528
;       INFORMATION FOR SEQ ID NO: 6:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 157 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          FEATURE:
;            OTHER INFORMATION: "Xaa" in position 73 is either
;            'Ile' or 'Thr'
;          SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

  Query Match           99.8%;  Score 810;  DB 4;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 11
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
;   APPLICANT: TANIMOTO, Tadao
;   APPLICANT: KURIMOTO, Masashi
;   TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BROWDY AND NEIMARK
;     STREET: 419 Seventh Street, N.W., Suite 300
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/896,605A
;     FILING DATE: 18 July 1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 207,691/1996
;     FILING DATE: 19-JUL-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 156,062/1997
;     FILING DATE: 30-MAY-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BROWDY, Roger L.
;     REGISTRATION NUMBER: 25,618
;     REFERENCE/DOCKET NUMBER: TANIMOTO=2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-628-5197
;     TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 193 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-896-605A-2

  Query Match           99.8%;  Score 810;  DB 2;  Length 193;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 12
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
;   APPLICANT: TANIMOTO, Tadao
;   APPLICANT: KURIMOTO, Masashi
;   TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BROWDY AND NEIMARK
;     STREET: 419 Seventh Street, N.W., Suite 300
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/896,501A
;     FILING DATE: 18-JUL-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 213,267/1996
;     FILING DATE: 25-JUL-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 31,474/1997
;     FILING DATE: 31-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BROWDY, Roger L.
;     REGISTRATION NUMBER: 25,618
;     REFERENCE/DOCKET NUMBER: TANIMOTO=3
;   TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-896-501A-2

  Query Match             99.8%;  Score 810;  DB 2;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 13
US-08-832-180-9
; Sequence 9, Application US/08832180
; Patent No. 6214584
;  GENERAL INFORMATION:
;    APPLICANT:  KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
;    APPLICANT:  KENKYUJO
;    APPLICANT:  USHIO, Shimpei
;    APPLICANT:  TORIGOE, Kakuji
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  OKAMURA, Haruki
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  INTERFERON-  PRODUCTION INDUCING
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect Version 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,180
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/558,191
;      FILING DATE:
;      APPLICATION NUMBER:  JP 304,203/94
;      FILING DATE:  No. 6214584ember 15, 1994
;      APPLICATION NUMBER:  10048102
;      FILING DATE:  September 18, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  USHIO=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-832-180-9

  Query Match             99.8%;  Score 810;  DB 4;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-88;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 14
US-09-597-576-2
; Sequence 2, Application US/09597576
; Patent No. 6432678
; GENERAL INFORMATION:
;  APPLICANT:  Alexander Taylor
;  APPLICANT:  Han Trinh
;  TITLE OF INVENTION:  MACACA CYNOMOLGUS IL18
;  FILE REFERENCE:  GP-70629
;  CURRENT APPLICATION NUMBER: US/09/597,576
;  CURRENT FILING DATE:  2000-06-20
;  PRIOR APPLICATION NUMBER:  60/140,140
;  PRIOR FILING DATE:  1999-06-21
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

  Query Match             97.5%;  Score 792;  DB 4;  Length 193;
  Best Local Similarity   95.5%;  Pred. No. 5.7e-86;
  Matches  150;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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Db     157 EGYFLACEKERDLYKLILKKKDELGDRSIMFTVQNED 193


RESULT 15
US-08-502-535B-2
; Sequence 2, Application US/08502535B
; Patent No. 5912324
;  GENERAL INFORMATION:
;    APPLICANT:  OKAMURA, Haruki
;    APPLICANT:  TANIMOTO, Tadao
;    APPLICANT:  TORIGOE, Kakuji
;    APPLICANT:  KUNIKATA, Toshio
```

```
;    APPLICANT:  TANIGUCHI, Mutsuko
;    APPLICANT:  KOHNO, Keizo
;    APPLICANT:  KURIMOTO, Masashi
;    TITLE OF INVENTION:  IFN-BETA PRODUCTION INDUCING PROTEIN AND
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY OF THE SAME
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
       APPLICATION NUMBER:  US/08/502,535B
       FILING DATE:  14-JUL-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 184162/1994
;      FILING DATE:  14-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 45057/1995
;      FILING DATE:  10-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  OKAMURA-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-502-535B-2

  Query Match             63.2%;  Score 513;  DB 2;  Length 157;
  Best Local Similarity   64.9%;  Pred. No. 4.3e-53;
  Matches  100;  Conservative   26;  Mismatches   26;  Indels    2;  Gaps    2;

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Job time : 15 secs
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 11:01:31 ; Search time 34 Seconds
(without alignments)
282.305 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	811	99.9	157	9	US-10-094-153-2	Sequence 2, Appli
2	811	99.9	157	10	US-09-775-046-9	Sequence 9, Appli
3	811	99.9	157	12	US-10-100-057-6	Sequence 6, Appli
4	811	99.9	193	9	US-09-770-528-8	Sequence 8, Appli
5	811	99.9	193	10	US-09-798-075-1	Sequence 1, Appli
6	810	99.8	157	10	US-09-924-099-21	Sequence 21, Appl
7	807	99.4	157	9	US-10-094-153-10	Sequence 10, Appl
8	807	99.4	193	9	US-10-094-153-9	Sequence 9, Appli
9	805	99.1	157	9	US-10-094-153-6	Sequence 6, Appli
10	805	99.1	157	9	US-10-094-153-7	Sequence 7, Appli
11	805	99.1	193	9	US-10-094-153-3	Sequence 3, Appli
12	805	99.1	193	9	US-10-094-153-4	Sequence 4, Appli
13	801	98.6	157	12	US-10-100-057-20	Sequence 20, Appl
14	799	98.4	157	9	US-10-094-153-8	Sequence 8, Appli
15	799	98.4	193	9	US-10-094-153-5	Sequence 5, Appli
16	791	97.4	157	12	US-10-100-057-21	Sequence 21, Appl
17	791	97.4	157	12	US-10-100-057-22	Sequence 22, Appl
18	782	96.3	157	12	US-10-100-057-25	Sequence 25, Appl
19	781	96.2	157	12	US-10-100-057-23	Sequence 23, Appl
20	772	95.1	157	12	US-10-100-057-26	Sequence 26, Appl
21	771	95.0	157	12	US-10-100-057-24	Sequence 24, Appl
22	634	78.1	157	10	US-09-917-265-12	Sequence 12, Appl
23	634	78.1	192	10	US-09-917-265-8	Sequence 8, Appli
24	610	75.1	154	10	US-09-917-265-5	Sequence 5, Appli
25	517	63.7	157	12	US-10-100-057-27	Sequence 27, Appl
26	515	63.4	157	10	US-09-775-046-8	Sequence 8, Appli
27	515	63.4	157	12	US-10-100-057-7	Sequence 7, Appli
28	515	63.4	192	9	US-09-770-528-9	Sequence 9, Appli
29	513	63.2	157	10	US-09-924-099-22	Sequence 22, Appl
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31	359	44.2	133	10	US-09-917-265-2	Sequence 2, Appli
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33	81	10.0	265	10	US-09-815-242-5859	Sequence 5859, Ap
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35	79	9.7	452	10	US-09-881-752A-268	Sequence 268, App
36	74	9.1	467	10	US-09-374-579-2	Sequence 2, Appli
37	71.5	8.8	467	10	US-09-374-579-4	Sequence 4, Appli
38	71.5	8.8	831	10	US-09-864-761-48702	Sequence 48702, A
39	71	8.7	14	12	US-10-100-057-12	Sequence 12, Appl
40	70	8.6	4590	9	US-10-160-758-13	Sequence 13, Appl
41	70	8.6	4590	9	US-10-160-758-14	Sequence 14, Appl
42	69.5	8.6	6304	9	US-10-147-026-16	Sequence 16, Appl
43	69	8.5	98	9	US-09-970-033-2	Sequence 2, Appli
44	68.5	8.4	331	10	US-09-924-841-4	Sequence 4, Appli
45	68.5	8.4	521	9	US-09-820-843A-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-10-094-153-2
; Sequence 2, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-153-2

Query Match 99.9%; Score 811; DB 9; Length 157;
Best Local Similarity 99.4%; Pred. No. 1.6e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1

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; GENERAL INFORMATION:
;  APPLICANT: Debets, Johannes Eduard Maria Antonius
;  APPLICANT:  Timans, Jacqueline C.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX01073K
;  CURRENT APPLICATION NUMBER: US/09/775,046
;  CURRENT FILING DATE:  2001-02-01
;  PRIOR APPLICATION NUMBER: 60/179,638
;  PRIOR FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-775-046-9

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  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 3
US-10-100-057-6
; Sequence 6, Application US/10100057
; Patent No. US20020150555A1
;   GENERAL INFORMATION:
;        APPLICANT: GILLISPIE, Matthew Todd
;                   HORWOOD, Nicole Joy
;                   UDAGAWA, No. US20020150555A1uyuki
;                   KURIMOTO, Masashi
;        TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Patent In Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/100,057
;             FILING DATE: 19-Mar-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/030,061
;             FILING DATE: 25-FEB-1998
;             APPLICATION NUMBER: JP 55,468/1997
;             FILING DATE: 25-FEB-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: GILLISPIE-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 628-5197
;             TELEFAX: (202) 737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 157 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6

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Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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RESULT 4
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; Sequence 8, Application US/09770528
; Patent No. US20020164332A1
;   GENERAL INFORMATION:
;        APPLICANT: Hedrick, Joseph A.
;                   Sana, Theodore R.
;                   Bazan, Fernando J.
;                   Kastelein, Robert A.
;        TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
;                            and Methods
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/770,528
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/130,972
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 60/055,111
;             FILING DATE: 06-AUG-1997
;             APPLICATION NUMBER: US 09/062,866
;             FILING DATE: 20-APR-1998
;             APPLICATION NUMBER: US 09/097,976
;             FILING DATE: 16-JUN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0725K2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-852-9196
;             TELEFAX: 650-496-1200
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
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  Best Local Similarity   99.4%;  Pred. No. 2.1e-75;
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Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 5
US-09-798-075-1
; Sequence 1, Application US/09798075
; Patent No. US20010044418A1
; GENERAL INFORMATION:
;  APPLICANT:  Levy, Shoshana
;  APPLICANT:  DeKryuff, Rosemarie
;  APPLICANT:  Umetsu, Dale
;  APPLICANT:  Maecker, Holden
;  TITLE OF INVENTION:  Treatment of Allergies
;  FILE REFERENCE:  STAN-179
;  CURRENT APPLICATION NUMBER: US/09/798,075
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER:  60/188,311
;  PRIOR FILING DATE:  2000-03-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-798-075-1

  Query Match             99.9%;  Score 811;  DB 10;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-75;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
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Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 6
US-09-924-099-21
; Sequence 21, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
;  APPLICANT: NISHIDA, Yoshihiro
;  APPLICANT:  OKURA, Takanori
;  APPLICANT:  TANIMOTO, Tadao
;  APPLICANT:  KURIMOTO, Masashi
;  TITLE OF INVENTION: PEPTIDE
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/924,099
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 21
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (73)
;   OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.
US-09-924-099-21

  Query Match             99.8%;  Score 810;  DB 10;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-75;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 7
US-10-094-153-10
; Sequence 10, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-10

  Query Match             99.4%;  Score 807;  DB 9;  Length 157;
  Best Local Similarity   98.7%;  Pred. No. 4.2e-75;
  Matches  155;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLKSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
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Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
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Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 8
US-10-094-153-9
; Sequence 9, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
   PRIOR FILING DATE: 2001-03-08
   NUMBER OF SEQ ID NOS: 18
   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-9

  Query Match           99.4%;  Score 807;  DB 9;  Length 193;
  Best Local Similarity   98.7%;  Pred. No. 5.4e-75;
  Matches  155;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 YFGKLKSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 9
US-10-094-153-6
; Sequence 6, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-6

  Query Match           99.1%;  Score 805;  DB 9;  Length 157;
  Best Local Similarity   98.7%;  Pred. No. 6.7e-75;
  Matches  155;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFGKLASKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 10
US-10-094-153-7
; Sequence 7, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-7

  Query Match           99.1%;  Score 805;  DB 9;  Length 157;
  Best Local Similarity   98.7%;  Pred. No. 6.7e-75;
  Matches  155;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYADSQPRGM 60

Qy     61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
          |||||||||||||||||||||||||||||||||||||
Db    121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 11
US-10-094-153-3
; Sequence 3, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-3

  Query Match             99.1%;  Score 805;  DB 9;  Length 193;
  Best Local Similarity   98.7%;  Pred. No. 8.7e-75;
  Matches  155;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLASKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 12
US-10-094-153-4
; Sequence 4, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-4

  Query Match             99.1%;  Score 805;  DB 9;  Length 193;
  Best Local Similarity   98.7%;  Pred. No. 8.7e-75;
  Matches  155;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYADSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 13
US-10-100-057-20
; Sequence 20, Application US/10100057
; Patent No. US20020150555A1
;   GENERAL INFORMATION:
;        APPLICANT: GILLISPIE, Matthew Todd
;                   HORWOOD, Nicole Joy
;                   UDAGAWA, No. US20020150555A1uyuki
;                   KURIMOTO, Masashi
;        TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Patent In Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/100,057
;             FILING DATE: 19-Mar-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/030,061
;             FILING DATE: 25-FEB-1998
;             APPLICATION NUMBER: JP 55,468/1997
;             FILING DATE: 25-FEB-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: GILLISPIE-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 628-5197
;             TELEFAX: (202) 737-3528
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 157 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-100-057-20

  Query Match             98.6%;  Score 801;  DB 12;  Length 157;
  Best Local Similarity   98.7%;  Pred. No. 1.7e-74;
  Matches  155;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKSEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 14
US-10-094-153-8
; Sequence 8, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-8
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  Query Match             98.4%;  Score 799;  DB 9;  Length 157;
  Best Local Similarity   98.1%;  Pred. No. 2.8e-74;
  Matches  154;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1 YFGKLASKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYADSQPRGM 60

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157


RESULT 15
US-10-094-153-5
; Sequence 5, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
;  APPLICANT: Dinarello, Charles
;  APPLICANT:  Kim, Soo Hyun
;  TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
;  FILE REFERENCE: 475
;  CURRENT APPLICATION NUMBER: US/10/094,153
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/274,327
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-5

  Query Match             98.4%;  Score 799;  DB 9;  Length 193;
  Best Local Similarity   98.1%;  Pred. No. 3.5e-74;
  Matches  154;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      37 YFGKLASKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYADSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


Search completed: April  4, 2003, 11:09:43
Job time : 35 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:58:21 ; Search time 17 Seconds
(without alignments)
887.830 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	515	63.4	192	2	S60226	cytokine IGIF - mo
2	85	10.5	381	2	T40341	hypothetical prote
3	82	10.1	263	2	T39487	hypothetical prote
4	81.5	10.0	270	1	S10532	interleukin-1 alph
5	80.5	9.9	866	2	C71509	probable DNA polym
6	79	9.7	452	2	D64583	hypothetical prote
7	78.5	9.7	204	2	T44357	hypothetical prote
8	78	9.6	473	2	T32038	hypothetical prote
9	77.5	9.5	1251	2	A56677	neuronal cell cycl
10	77	9.5	364	2	A81261	probable periplasm
11	76	9.4	632	2	T00679	hypothetical prote
12	76	9.4	747	2	E84698	hypothetical prote
13	75.5	9.3	192	2	S15661	(2'-5')oligo(A) sy
14	75.5	9.3	270	2	I46620	interleukin-1 alph
15	75.5	9.3	1036	2	H64245	hypothetical prote
16	75.5	9.3	1663	1	C3MS	complement C3 prec
17	75	9.2	1064	1	S57450	protein-tyrosine k
18	75	9.2	2470	2	I50726	cation-independent
19	74.5	9.2	334	2	T04198	hypothetical prote
20	74.5	9.2	389	2	B69277	TRK potassium upta
21	74.5	9.2	467	2	A48713	serine/threonine-s
22	74.5	9.2	1228	2	A57384	multimerin, endoth
23	74.5	9.2	1510	2	T16927	hypothetical prote
24	74	9.1	245	2	B90488	hypothetical prote
25	74	9.1	361	2	E96904	minD family ATPase
26	74	9.1	376	2	T24925	hypothetical prote
27	74	9.1	467	2	I49609	proto-oncogene pro
28	74	9.1	467	2	A47388	serine/threonine p
29	74	9.1	680	2	A28121	major merozoite su
30	74	9.1	810	2	B71639	virb4 protein prec
31	74	9.1	1772	2	A45532	major merozoite su
32	73.5	9.1	268	2	H85641	probable small sub
33	73.5	9.1	268	2	C90781	probable small sub
34	73	9.0	418	2	D82932	seryl-tRNA synthet
35	73	9.0	447	2	T26293	hypothetical prote
36	72.5	8.9	268	1	B24073	interleukin-1 alph
37	72.5	8.9	313	2	C96528	protein F27J15.10
38	72.5	8.9	436	2	G97701	polynucleotide ade
39	72.5	8.9	475	2	T32036	hypothetical prote
40	72.5	8.9	888	2	A38539	p101 protein precu
41	72.5	8.9	1246	2	S60954	probable membrane
42	72.5	8.9	1294	2	T48349	EIN2 protein - Ara
43	72.5	8.9	1997	2	F71607	DNA helicase II BR
44	72	8.9	264	2	B90051	hypothetical prote
45	72	8.9	1613	2	S39059	protein BRG1 - hum

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: S60226
R;Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
.
Nature 378, 88-91, 1995
A;Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A;Reference number: S60226; MUID:96061009; PMID:7477296
A;Accession: S60226
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <OKA>
A;Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823
C;Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;
Best Local Similarity 64.9%; Pred. No. 2.7e-42;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

```
Qy       2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMA 61
           ||:|    :||||:||||||:|:  :|:|||||| |   : |:|  || |||||: ||:|
Db      37 FGRLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLA 95

Qy      62 VTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYE 121
           ||:|||  |:| |||:||||||:||:||:|| | :||:|||| |||| |||:|||| ||
Db      96 VTLSVKDSKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy     122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
           |:||||:|| | |||||||:|| ||:|:|||: |
Db     155 GHFLACQKEDDAFKLILKKKDENGDKSVMFTLTN 188
```

RESULT 2
T40341
hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40341
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z21922
A;Accession: T40341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-381 <WOO>
A;Cross-references: EMBL:AL022070; PIDN:CAA17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c
A;Experimental source: strain 972h-; cosmid c3B9
C;Genetics:
A;Gene: SPDB:SPBC3B9.02c

A;Map position: 2

Query Match 10.5%; Score 85; DB 2; Length 381;
Best Local Similarity 26.4%; Pred. No. 1.6;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

```
Qy       3 GKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAV 62
           |:| || :   ::| :  |:  | :|:  ::|: |   |  :|:|
Db     208 GQLSSKDAF--DVNQRPTFLGMGAKPVDSELTELDIWKNPKKTMF-------------- 250

Qy      63 TISVK-CEKISXLSCENKIISF-KEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
             : ||  |  | |: :|:     |: |  ||:  | |  :| :||    || :  |||
Db     251 -LPVKPLESNSALNSQNEHTEVQKKSNSIDNL--TPSSELFRKRS---RDNNLSRESS-- 302

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRS 148
                 |  |       | |   ||:
Db     303 -----VSSKHLDYNSRNYNKRDRDPDRT 325
```

RESULT 3
T39487
hypothetical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T39487
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21858
A;Accession: T39487
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-263 <LYN>
A;Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c
A;Experimental source: strain 972h-; cosmid c15D4
C;Genetics:
A;Gene: SPDB:SPBC15D4.11c
A;Map position: 2
A;Introns: 96/2; 147/3
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

```
Qy       4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVT 63
           ||:|:|  :: : |: |      : |   :   |       ::  ||  |::    : ||
Db      47 KLDSELGYVKQVLDETLPKKGYEKALHSFIIHED------PSLNYISALKETAKERIRVT 100

Qy      64 ISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGH-------------- 109
           : |   : | :  : | |:     |  :|  :|  :::||| |:| :
Db     101 VPVYSSRKSYV--QTKPITHSAEN--ENGNETSDELVFFQHSIPAYVQLTNNHGTILCAL 156

Qy     110 ---DNKMQFESSSYEGYFLACEKERDLFKLILKKEDELGDR 147
                 : |:| |::    :     || :|||:|  :   |
Db     157 ILCKGMLHFDSISFQSPQNSQAFSSDL-RLILQKSQKYTGR 196
```

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N;Alternate names: hematopoietin-1; IL-1 alpha
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
C;Accession: S10532
R;Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.
Nucleic Acids Res. 18, 4282, 1990
A;Title: Porcine IL-1 alpha cDNA nucleotide sequence.
A;Reference number: S10532; MUID:90332454; PMID:2377484
A;Accession: S10532
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <MAL>
A;Cross-references: EMBL:X52731; NID:g1987; PIDN:CAA36945.1; PID:g1988
C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte p

C;Comment: IL-1 proteins are involved in the inflammatory response, being identified
lls.
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1alpha, unlike interleukin-1beta, is fully active.
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F;1-112/Domain: propeptide #status predicted <PRO>
F;113-270/Product: interleukin-1 alpha #status predicted <IL1>
F;82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 2.3;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

```
Qy       8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMAV 62
           | : :| :| | :  |  |: :  | :      :   :|    : | :: |  :    : |
Db     123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAAVLNNLDEAVKFDMAAYTSNDDSQLPV 182

Qy      63 TISVKCEKISXLSCEN--KIISFKEM-NPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSS 119
           |: :  |    :| :|  : :  ||:   |  |||  | : |:::    | |   |:|::
Db     183 TLRIS-ETRLFVSAQNEDEPVLLKELPETPKTIKDETSLLFFWEK----HGNMDYFKSAA 237

Qy     120 YEGYFLACEKER 131
           :   |:|  :|:
Db     238 HPKLFIATRQEK 249
```

RESULT 5
C71509
probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: C71509
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-866 <ARN>
A;Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC68093.1; PID:g332
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: polA
C;Superfamily: DNA-directed DNA polymerase I

Query Match 9.9%; Score 80.5; DB 2; Length 866;
Best Local Similarity 26.4%; Pred. No. 11;
Matches 34; Conservative 22; Mismatches 28; Indels 45; Gaps 8;

```
Qy       1 YFGKLESKLSVIRNLNDQVLFI---DQGNRPLFEDMTD--------SDCRDNAPRTIFII 49
           ||| | |||  |:|     ||:   ::| : :|| :           :|          :
Db     441 YFGMLASKLLAIKN----YLFVKLEEKGLKDIFETVEQPLEAVLFAMEC----------V 486

Qy      50 SMYKDSQPRGMAV---TISVKCEKIS-----XLSCENKIISFKEMN----------PPDN 91
             |  |||  |:||    :: : |: |       : ||  | | |:::          | |
Db     487 GMPLDSQ--GLAVLDRDLTKELEECSQEIYDLVGCEFNIKSPKQLSDILYQRLGIEPVDK 544

Qy      92 IKDTKSDII 100
           | ||::::
Db     545 AKSTKAEVL 553
```

RESULT 6
D64583
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: D64583
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64583
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-452 <TOM>
A;Cross-references: GB:AE000565; GB:AE000511; NID:g2313616; PIDN:AAD07578.1; PID:g231362

Query Match 9.7%; Score 79; DB 2; Length 452;
Best Local Similarity 23.8%; Pred. No. 7.4;
Matches 40; Conservative 30; Mismatches 72; Indels 26; Gaps 8;

```
Qy      9 LSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPR---------- 58
          |   |  |:|  |:   |  |:| :  ::   |   :  :::      |:
Db    105 LVYFRQFNNQA-FLIAPNDELYEQIRATNTDINFISSDLLVTFLNGFDPKIANLRKACNV 163

Qy     59 -GMAVTISVKCEKISXLSCEN-KIISFKEMNPPDNIKDTKSDIIFFQRSVPGHD----NK 112
           : |   |    :: ||||: :|:  :|:   |    ||:   || | | | |     |
Db    164 YSVGVIYIVTTNTLNILSCESFEILEKREL---DTSGVTKTSTPFFSR-VEGIDAGTLGK 219

Qy    113 MQFESSSYEGYF----LACEKERDLFKLILKKEDELGDRSIMFTVQNE 156
          : |  |  : ||       :||:     | |:|:::  | |   :: |
Db    220 L-FSGSQSKNYFAYYDALVKKEKRKEVRIKKREEKIDSREIKREIKQE 266
```

RESULT 7
T44357
hypothetical protein [imported] - Clostridium histolyticum
C;Species: Clostridium histolyticum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44357
R;Matsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A;Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A;Reference number: Z22752; MUID:99121032; PMID:9922257
A;Accession: T44357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-204 <MAT>
A;Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BAA34544.1; PID:g3892648
A;Experimental source: strain JCM 1403

Query Match 9.7%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 3.2;
Matches 32; Conservative 19; Mismatches 51; Indels 19; Gaps 5;

```
Qy      9 LSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFII--SMYKDSQPRGMAVTISV 66
          :|   | | :     ||     | :      ||:  :| |:  |:|   :      |:
Db     25 ISTFENRNHKASSNKQGEAKTGEKIN----IDNSSNSIKIVYESVYLKPEGEQNKTTVDE 80

Qy     67 KCEK-------ISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSS 119
            ||      || :: |  :  ||: :   |:|| | | | | ||:    || :::
Db     81 CIEKFNKDKKVISDMTKEQVLAVFKKHD--YNLKDIKKDQIVFSRSI----NKYKYQEGK 134

Qy    120 Y 120
          |
Db    135 Y 135
```

RESULT 8
T32038
hypothetical protein F41B5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Feb-2001
C;Accession: T32038
R;Dante, M.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F41B5.
A;Reference number: Z21115
A;Accession: T32038
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-473 <DAN>
A;Cross-references: EMBL:AF016676; PIDN:AAC25900.1; GSPDB:GN00023; CESP:F41B5.2
A;Experimental source: strain Bristol N2; clone F41B5
C;Genetics:
A;Gene: CESP:F41B5.2
A;Map position: 5
A;Introns: 67/1; 233/2; 403/3
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;298-461/Domain: cytochrome P450 homology <P45>
F;439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 9.6%; Score 78; DB 2; Length 473;
Best Local Similarity 21.5%; Pred. No. 9.7;
Matches 32; Conservative 28; Mismatches 57; Indels 32; Gaps 6;

```
Qy     10 SVIRNLNDQVLF---IDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISV 66
          : | |: :| :|    |: |:  :: :                :  ::::      ||: |
Db    170 NAIANVINQTIFGYRFDESNQEEYKKLKH------------LIEFQENVFTSAKVTVQV 216

Qy     67 KCEKISXLSCENKIISFKEMNPPDNIKDTKSDII-FFQRSVPGHDNKMQFESSSYEGYFL 125
             |:       ||:  : :   |:||  |:    ||   :  |  |: |:|   : |
Db    217 FAPKL------GKILPGESLE--DLMKDWKNSFYDFFNTQIENHRQKIDFDSEESQDYAE 268

Qy    126 ACEKERDLFKLILKKEDELGDRSIMFTVQ 154
          |  ||:       || : |||  :    |
Db    269 AYLKEQ-------KKYEALGDTELFSNKQ 290
```

RESULT 9
A56677
neuronal cell cycle withdrawal protein QN1 - quail (fragment)
C;Species: Coturnix coturnix (quail)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
C;Accession: A56677
R;Bidou, L.; Crisanti, P.; Blancher, C.; Pessac, B.
Mech. Dev. 43, 159-173, 1993
A;Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic n
A;Reference number: A56677; MUID:94128599; PMID:8297788
A;Accession: A56677
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1251 <BID>
A;Cross-references: GB:S68151; NID:g545153; PIDN:AAD14007.1; PID:g4261707
A;Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 34;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;

```
Qy      6 ESKLSVI-RNLNDQVLFI---DQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMA 61
            | ||: | : : || : |    | |  |:: | |   ::          |||::|   |:
Db    648 EEKLAQIQKEMEDQEVIIQGYQQENERLYKQMKDLQIQNKKNEE----QMYKENQCL-MS 702

Qy     62 VTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFE----- 116
            |::: ||:  :: :::|:  :|  |  |   : :::|   |:    : |:: |
Db    703 ELIALR-EKVERINIQSQIV--RESEPARN--QSFTELISELRAARKEETKLREEIRRLK 757

Qy    117 --SSSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 156
             : |      :|||| |: :       ::|  | :  |
Db    758 QDKQALELDLGQAKKERDLAKVQITSTS--SEKSYEFKIMEE 797
```

RESULT 10
A81261
probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: A81261
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil

```
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81261
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <PAR>
A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1643

  Query Match             9.5%;  Score 77;  DB 2;  Length 364;
  Best Local Similarity   24.8%;  Pred. No. 8.9;
  Matches   38;  Conservative   21;  Mismatches   40;  Indels   54;  Gaps    9;

Qy      12 IRNLNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTIFIISMYK----DSQPR-------- 58
           :| ||:::|| |:|:   |: : |:   | |    :|   : |    ||:|:
Db     211 LRKLNEKILFADRGSTLYFQVLRDN--MDLNISTEVFAKDLSKFNLPDSKPKPKITNFTS 268

Qy      59 --GMAVTISVKCEKI---------------SXLSCENKII-SFKEMNPPDNI-------- 92
             |: |  |:   ||                |   | |: :|||:    ||
Db     269 NLGLTVNASLVVTKIDPKSKVSNAGFMVGDKILRVNNIILNNFKEL---QNILSAGNDFS 325

Qy      93 -----KDTKSDIIFFQRSVPGH-----DNKMQF 115
                | ||  :  |   : |:     | | ||
Db     326 ILIERKSTKLPLSNFNNELGGNANSGGDGKFQF 358


RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F6E13.12
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00679; A84873
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A;Reference number: Z14180
A;Accession: T00679
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-632 <ROU>
A;Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84873
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-632 <STO>
A;Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g43990; F6E13.12
A;Map position: 2

  Query Match             9.4%;  Score 76;  DB 2;  Length 632;
  Best Local Similarity   25.6%;  Pred. No. 21;
  Matches   34;  Conservative   29;  Mismatches   40;  Indels   30;  Gaps    9;

Qy      28 PLFEDMTDSD-CRDNAPRTIFIISMYKDSQPRGMAVTISVKCEK-------ISXLSCENK 79
           || :    || |  :: |::  : :||::  |   :: |:   :        |   ||: :
Db     368 PLSDRSASSDLCNISSGRSLSPMDIYKETTRR---ISSSLSPNELFRFRRRFIHLSSCDGE 424

Qy      80 IISFK-----EMNPPDNIKDTKSDIIFFQRSVP--GHDNKMQF--ESSSYEGYF-LACEK 129
             :|      |::| :::|  ||  :    ||   | :| :|    :||:: || |:| :
Db     425 ASAFDTSPTCELDPSEHLKGDKSSPL----SVDTLGSENVIQTPESNSSFDNYFGLSCSQ 480

Qy     130 ERDLFKLILKKED 142
                  | || |
Db     481 AE-----IQKKHD 488


RESULT 12
E84698
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84698
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84698
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-747 <STO>
A;Cross-references: GB:AE002093; NID:g3582336; PIDN:AAC35233.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g29620
A;Map position: 2

  Query Match             9.4%;  Score 76;  DB 2;  Length 747;
  Best Local Similarity   24.7%;  Pred. No. 26;
  Matches   36;  Conservative   29;  Mismatches   59;  Indels   22;  Gaps    7;

Qy       4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVT 63
           ||: : || ||   :|         : :|   |   ::    : : ::| :  |     |
Db     102 KLKHQQSVRRNARRKV-------EEVGKDWDSSQASEDERGKVILTTLYGEVLPE----T 150

Qy      64 ISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQR--SVPGHDNKMQFE---SS 118
           |:   ||       : :   | |  |:: |   |::  :|  || | |:: : |   ||
Db     151 ITPDMEKFK----RERTLLVAEENVFDSVLDNHRDLVELERLISVDG-DDESEVECSSSS 205

Qy     119 SYEGYFLACEKERDLFKLILK-KEDE 143
           | ||     |:  |: |:::   ||:
Db     206 SSEGEKEEEERREDVSKVVVAWTEDD 231


RESULT 13
S15661
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999
C;Accession: S15661; S19108
R;Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.
Nucleic Acids Res. 19, 1917-1924, 1991
A;Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked
A;Reference number: S15660; MUID:91232962; PMID:1709495
A;Accession: S15661
A;Molecule type: mRNA
A;Residues: 1-192 <RUT>
A;Cross-references: EMBL:X55982
R;Williams, B.
submitted to the EMBL Data Library, September 1990
A;Reference number: S19108
A;Accession: S19108
A;Molecule type: mRNA
A;Residues: 1-175,'L',177-192 <WIL>
A;Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715
C;Superfamily: oligo(A) synthetase
C;Keywords: nucleotidyltransferase

  Query Match             9.3%;  Score 75.5;  DB 2;  Length 192;
  Best Local Similarity   23.2%;  Pred. No. 5.8;
  Matches   42;  Conservative   24;  Mismatches   50;  Indels   65;  Gaps    9;

Qy       3 GKLESKLSVIRN--------LNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKD 54
```

```
          |: :: | |  |        || | : | :  : | |   :  |
Db     11 GRSDADLVVFLNNLTSFEDQLNQQGVLIKEIKKQLCEVQHERRC---------------- 54

Qy     55 SQPRGMAVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDII-------------- 100
                  || |  |  |  :: :||| :: || :|: | |::
Db     55 ----------GVKFEVHSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLLDHLNILKK 103

Qy    101 ----FFQR---SVP-GHDNKMQFESSSYEGYFLACE--KERDLFKLI-----LKKEDELG 145
           |:      || | : |:       : ||| |   | : | :|:     | || :||
Db    104 PNQQFYANLISGVPAGKEGKLSICFMGLQKYFLNCRPTKLKRLIRLVTHWYQLCKE-KLG 162

Qy    146 D 146
           |
Db    163 D 163


RESULT 14
I46620
interleukin-1 alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000
C;Accession: I46620
R;Maliszewski, C.
Nucleic Acids Res. 14, 4282, 1990
A;Title: Nucleotide sequence of porcine interleukin-1 alpha.
A;Reference number: I46620
A;Accession: I46620
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-270 <MAL>
A;Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623
C;Superfamily: interleukin-1
C;Keywords: lipoprotein; myristylation
F;1-112/Domain: propeptide #status predicted <PRO>
F;113-270/Product: interleukin-1 alpha #status predicted <IL1>
F;82,83/Binding site: myristate (Lys) (covalent) #status predicted

  Query Match             9.3%;  Score 75.5;  DB 2;  Length 270;
  Best Local Similarity   22.0%;  Pred. No. 8.7;
  Matches   29;  Conservative   32;  Mismatches   58;  Indels   13;  Gaps    6;

Qy      8 KLSYIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMAV 62
          | : :| :| | :  |  |: :  | :     :   :|    : | :: |  :    : |
Db    123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAAVLNNLDEAVKFDMAAYTSNDDSQLPV 182

Qy     63 TISVKCEKISXLSCEN--KIISFKEM-NPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSS 119
          |: :  |    :| :|  : :  ||:   |  |||  | : |:::    | |   |:|::
Db    183 TLRIS-ETRLFVSAQNEDEPVLLKELPETPKTIKDETSLLFFWEK----HGNMDYFKSAA 237

Qy    120 YEGYFLACEKER 131
          :    :|  :|:
Db    238 HPKLLIATRQEK 249


RESULT 15
H64245
hypothetical protein MG414 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
C;Accession: H64245; G64245
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64245
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1036 <TIGR>
A;Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414
A;Experimental source: strain G-37
A;Accession: G64245
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',310-1036 <TIG2>
A;Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: hypothetical protein MG413

  Query Match             9.3%;  Score 75.5;  DB 2;  Length 1036;
  Best Local Similarity   21.9%;  Pred. No. 43;
  Matches   33;  Conservative   32;  Mismatches   65;  Indels   21;  Gaps    6;

Qy     14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEK- 70
          :|||: | :|: |  | |    |  : | |      | : ::     :   : |: :|
Db    845 SLNDEQLLVDKLNITLSEKRLQTTKNVRFNLKNKFINIHLVENKNQFNLVFDVDVRSKKL 904

Qy     71 -ISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEK 129
           |  :: :|:: |        ::| | :  :       | || : |: :|        |
Db    905 FIKGVNNDNQVFSISY-----DLKITNNQTLLIV-DANGFDNSIWFDITS--------EN 950

Qy    130 ERDLFKLI---LKKEDELGDRSIMFTVQNED 157
          :  ||| :   ||: :    |   | ::::|
Db    951 QTQLFKALSFYLKQNNLQFKRVPDFNLKSQD 981


Search completed: April  4, 2003, 11:01:47
Job time : 20 secs
```

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:52:35 ; Search time 12 Seconds
(without alignments)
542.649 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	811	99.9	193	1	IL18_HUMAN	Q14116	homo sapien
2	659	81.2	193	1	IL18_HORSE	Q9xsq7	equus cabal
3	654	80.5	193	1	IL18_BOVIN	Q9tu73	bos taurus
4	637	78.4	192	1	IL18_PIG	O19073	sus scrofa
5	613	75.5	193	1	IL18_CANFA	Q9xsr0	canis famil
6	515	63.4	192	1	IL18_MOUSE	P70380	mus musculu
7	514.5	63.4	194	1	IL18_RAT	P97636	rattus norv
8	81.5	10.0	270	1	IL1A_PIG	P18430	sus scrofa
9	81	10.0	267	1	IL1A_RABIT	P04822	oryctolagus
10	77.5	9.5	674	1	MUTL_CLOPE	Q8x186	clostridium
11	76.5	9.4	270	1	IL1A_HORSE	Q28385	equus cabal
12	75.5	9.3	192	1	OASB_MOUSE	Q60856	mus musculu
13	75.5	9.3	1036	1	Y414_MYCGE	P47653	mycoplasma
14	75.5	9.3	1663	1	CO3_MOUSE	P01027	mus musculu
15	74.5	9.2	1228	1	ECM_HUMAN	Q13201	homo sapien
16	74	9.1	467	1	M3K8_MOUSE	Q07174	mus musculu
17	74	9.1	467	1	M3K8_RAT	Q63562	rattus norv
18	74	9.1	1772	1	MSP1_PLAYO	P13828	plasmodium
19	73	9.0	270	1	IL1A_FELCA	O46613	felis silve
20	73	9.0	426	1	YCXC_ASTLO	P58151	astasia lon
21	72.5	8.9	313	1	COL4_ARATH	Q9m9b3	arabidopsis
22	71.5	8.8	268	1	IL1A_BOVIN	P08831	bos taurus
23	71.5	8.8	467	1	M3K8_HUMAN	P41279	homo sapien
24	71.5	8.8	527	1	RAG2_HUMAN	P55895	homo sapien
25	71	8.7	700	1	NONA_DROME	Q04047	drosophila
26	70.5	8.7	245	1	KDSB_FUSNN	Q8rfa8	fusobacteri
27	70.5	8.7	268	1	IL1A_CAPHI	P79161	capra hircu
28	70.5	8.7	644	1	YGM4_YEAST	P53129	saccharomyc
29	70	8.6	198	1	VS11_ROTRA	P17467	rabbit rota
30	70	8.6	1647	1	SN24_HUMAN	P51532	homo sapien
31	70	8.6	2663	1	CENE_HUMAN	Q02224	homo sapien
32	70	8.6	4590	1	FATH_HUMAN	Q14517	homo sapien
33	69.5	8.6	268	1	IL1A_SHEEP	Q28579	ovis aries
34	69.5	8.6	351	1	RF1_TREPA	O83090	treponema p
35	69.5	8.6	375	1	YYC5_CAEEL	Q18610	caenorhabdi
36	69.5	8.6	582	1	CRTI_CAPAN	P80093	capsicum an
37	69.5	8.6	919	1	RPO2_CAPVK	P16716	capripoxvir
38	69.5	8.6	1091	1	ITA6_MOUSE	Q61739	mus musculu
39	69.5	8.6	2920	1	CLR2_MOUSE	Q9r0m0	mus musculu
40	69	8.5	492	1	UBID_PASMU	Q9cp43	pasteurella
41	69	8.5	516	1	YVNF_AZOCH	P24423	azotobacter
42	69	8.5	578	1	TRM1_DROME	Q9vk89	drosophila
43	68.5	8.4	270	1	IL1A_MOUSE	P01582	mus musculu
44	68.5	8.4	331	1	IPNS_PENCH	P08703	penicillium
45	68.5	8.4	706	1	YK70_YEAST	P36166	saccharomyc

ALIGNMENTS

RESULT 1
IL18_HUMAN
ID IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=Peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC ---
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D49950; BAA08706.1; -.
DR   EMBL; AF077611; AAC27787.1; -.
DR   EMBL; AY044641; AAK95950.1; -.
DR   EMBL; BC007007; AAH07007.1; -.
DR   EMBL; BC007461; AAH07461.1; -.
DR   EMBL; U90434; AAB50010.1; -.
DR   Genew; HGNC:5986; IL18.
DR   MIM; 600953; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
KW   Cytokine.
FT   PROPEP        1     36       BY SIMILARITY.
FT   CHAIN        37    193       INTERLEUKIN-18.
FT   CONFLICT     66     66       F -> L (IN REF. 2).
FT   CONFLICT     86     86       S -> R (IN REF. 2).
FT   CONFLICT    191    191       N -> S (IN REF. 2).
SQ   SEQUENCE   193 AA;  22326 MW;  323C62C203788D55 CRC64;

  Query Match             99.9%;  Score 811;  DB 1;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 1e-68;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||||||||||||||||||||||||||
Db     157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 2
IL18_HORSE
ID   IL18_HORSE     STANDARD;      PRT;   193 AA.
AC   Q9XSQ7;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18 OR IGIF.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11131; CAA72013.1; -.
KW   Cytokine.
FT   PROPEP        1     36       BY SIMILARITY.
FT   CHAIN        37    193       INTERLEUKIN-18.
SQ   SEQUENCE   193 AA;  22058 MW;  4D81535E9004ECAF CRC64;

  Query Match             81.2%;  Score 659;  DB 1;  Length 193;
  Best Local Similarity   77.7%;  Pred. No. 1.4e-54;
  Matches  122;  Conservative   21;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||:|| |||:||||||||||||:|||:|:|||| |||| ||||:|:||| |||||  ||:
Db      37 YFGRLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCTDNAPQTVFIIYMYKDSLTRGL 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||| | |||:||||||||||:||:|| |  :|||||||||||||:|:||||| |
Db      97 AVTISVKCEKTSTLSCKNKIISFKEMSPPENINDEGNDIIFFQRSVPGHDDKIQFESSLY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :||||||||| ||||||||::.|| ||:|:|||||::
Db     157 KGYFLACEKENDLFKLILKEKDENGDKSVMFTVQNQN 193


RESULT 3
IL18_BOVIN
ID   IL18_BOVIN     STANDARD;      PRT;   193 AA.
AC   Q9TU73;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20012648; PubMed=10547157;
RA   Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT   "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT   18 expression in macrophages and its IFN-gamma-inducing activity.";
RL   J. Interferon Cytokine Res. 19:1169-1177(1999).
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF124789; AAF08686.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
KW   Cytokine.
FT   PROPEP        1     36       BY SIMILARITY.
FT   CHAIN        37    193       INTERLEUKIN-18.
SQ   SEQUENCE   193 AA;  22347 MW;  65720F199DEA49C4 CRC64;

  Query Match             80.5%;  Score 654;  DB 1;  Length 193;
  Best Local Similarity   77.1%;  Pred. No. 4.2e-54;
  Matches  121;  Conservative   23;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           :||||| |||:||||||||||:|||:|:|||| |||| ||||:|||| |||||  ||:
Db      37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSDNAPQTIFIIYMYKDSLTRGL 96
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```
Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||:|:|:| |||||||:|||||||||| : :|||||||||||||:|:||||| |
Db      97 AVTISVQCKKMSTLSCENKIVSFKEMNPPDNIDNEESDIIFFQRSVPGHDDKIQFESSLY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :||||||:|| |||||||||:|:  |:|:||||||::
Db     157 KGYFLACKKENDLFKLILKKQDDNRDKSVMFTVQNQN 193


RESULT 4
IL18_PIG
ID   IL18_PIG       STANDARD;      PRT;   192 AA.
AC   O19073;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18 OR IGIF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Foss D.L., Murtaugh M.P.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Muneta Y., Mori Y.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Intestine;
RX   MEDLINE=20260994; PubMed=10803849;
RA   Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA   Oswald E., Oswald I.P.;
RT   "Cloning, chromosomal location, and tissue expression of the gene for
RT   pig interleukin-18.";
RL   Immunogenetics 51:358-365(2000).
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U68701; AAC18415.1; -.
DR   EMBL; AB010003; BAA24135.1; -.
DR   EMBL; AF191088; AAF71200.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
KW   Cytokine.
FT   PROPEP        1     35       BY SIMILARITY.
FT   CHAIN        36    192       INTERLEUKIN-18.
SQ   SEQUENCE   192 AA;  22026 MW;  881EA654E221A17A CRC64;

  Query Match             78.4%;  Score 637;  DB 1;  Length 192;
  Best Local Similarity   75.2%;  Pred. No. 1.6e-52;
  Matches  118;  Conservative   24;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||| |||:||||||||||:||:: :|||| |||| |||||:|:||| |||||  ||:
Db      36 YFGKLEPKLSIIRNLNDQVLFINQGHQAVFEDMPDSDCSDNAPQTVFIIYMYKDSLTRGL 95

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||:|:|:| |||:|| :|||||:|||| |  :|||||||||||||:|:||||| |
Db      96 AVTISVQCKKMSTLSCKNKTLSFKEMSPPDNIDDEGNDIIFFQRSVPGHDDKIQFESSLY 155

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :||||||:|| |||||||||::|| ||:||||||||::
Db     156 KGYFLACKKENDLFKLILKEKDECGDKSIMFTVQNKN 192


RESULT 5
IL18_CANFA
ID   IL18_CANFA     STANDARD;      PRT;   193 AA.
AC   Q9XSR0;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18 OR IGIF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Argyle D.J., McGillivery C., Nicolson L., Onions D.E.;
RT   "Cloning, sequencing and characterization of canine interleukin-18.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11133; CAA72015.1; -.
KW   Cytokine.
FT   PROPEP        1     36       BY SIMILARITY.
FT   CHAIN        37    193       INTERLEUKIN-18.
SQ   SEQUENCE   193 AA;  22037 MW;  0D973E586F461F25 CRC64;

  Query Match             75.5%;  Score 613;  DB 1;  Length 193;
  Best Local Similarity   73.7%;  Pred. No. 2.8e-50;
  Matches  115;  Conservative   23;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||| |||:||||||||||:::||:|:|||| |||| |||| ||||| |||||  ||:
Db      37 YFGKLEPKLSIIRNLNDQVLFVNEGNQPVFEDMPDSDCTDNAPHTIFIIYMYKDSLTRGL 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||| : :| |||:|| |||::|:|||:|  |  :|||||||||||||:|:||||| |
Db      97 AVTISVKYKTMSTLSCKNKTISFQKMSPPDSINDEGNDIIFFQRSVPGHDDKIQFESSLY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 156
           :|:||||:|| |||||||| :|| ||:||||||||:
Db     157 KGHFLACKKENDLFKLILKDKDENGDKSIMFTVQNK 192


RESULT 6
IL18_MOUSE
ID   IL18_MOUSE     STANDARD;      PRT;   192 AA.
AC   P70380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
```

```
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18 OR IGIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=96061009; PubMed=7477296;
RA   Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA   Tanimoto T., Torigoe K., Okura T., Nukada Y., Hattori K.,
RA   Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT   "Cloning of a new cytokine that induces IFN-gamma production by T
RT   cells.";
RL   Nature 378:88-91(1995).
RN   [2]
RP   SEQUENCE OF 1-191 FROM N.A.
RC   STRAIN=NOD; TISSUE=Pancreas;
RX   MEDLINE=97174346; PubMed=9022080;
RA   Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT   "Active stage of autoimmune diabetes is associated with the
RT   expression of a novel cytokine, IGIF, which is located near Idd2.";
RL   J. Clin. Invest. 99:469-474(1997).
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; D49949; BAA08705.1; -.
DR   EMBL; U66244; AAB49753.1; -.
DR   MGD; MGI:107936; Il18.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
KW   Cytokine.
FT   PROPEP        1     35
FT   CHAIN        36    192       INTERLEUKIN-18.
FT   CONFLICT    183    185       MFT -> IS (IN REF. 2).
SQ   SEQUENCE   192 AA;  22135 MW;  8FED938473874D63 CRC64;

  Query Match             63.4%;  Score 515;  DB 1;  Length 192;
  Best Local Similarity   64.9%;  Pred. No. 3.7e-41;
  Matches  100;  Conservative   27;  Mismatches   25;  Indels    2;  Gaps    2;

Qy       2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMA 61
           ||:|    :||||:||||||:|:  :|:|||||| |   : |:|  || |||||: ||:|
Db      37 FGRLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLA 95

Qy      62 VTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYE 121
           ||:|||  |:| |||:||||||:||:||:|| | :||:||||: |||| |||:|||| ||
Db      96 VTLSVKDSKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy     122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
           |:||||:|| | |||||||:|| ||:|:|||: |
Db     155 GHFLACQKEDDAFKLILKKKDENGDKSVMFTLTN 188


RESULT 7
IL18_RAT
ID   IL18_RAT       STANDARD;      PRT;   194 AA.
AC   P97636; P97637; O88749;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE   (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN   IL18 OR IGIF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX   MEDLINE=97152963; PubMed=8999896;
RA   Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT   "Induction of interferon-gamma inducing factor in the adrenal
RT   cortex.";
RL   J. Biol. Chem. 272:2035-2037(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=98368130; PubMed=9702748;
RA   Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT   "Cloning of rat brain interleukin-18 cDNA.";
RL   Mol. Psych. 3:362-366(1998).
CC   -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC       AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC       CELLS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U77776; AAC53009.1; -.
DR   EMBL; U77777; AAC53010.1; -.
DR   EMBL; AJ222813; CAA11001.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
KW   Cytokine; Alternative splicing.
FT   PROPEP        1     36       BY SIMILARITY.
FT   CHAIN        37    194       INTERLEUKIN-18.
FT   VARSPLIC    121    139       MISSING (IN ISOFORM ALPHA).
FT   CONFLICT      4      5       MS -> IP (IN REF. 2).
FT   CONFLICT     48     48       I -> M (IN REF. 2).
SQ   SEQUENCE   194 AA;  22303 MW;  E2089AD6F1798450 CRC64;

  Query Match             63.4%;  Score 514.5;  DB 1;  Length 194;
  Best Local Similarity   63.2%;  Pred. No. 4.2e-41;
  Matches   98;  Conservative   28;  Mismatches   28;  Indels    1;  Gaps    1;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
             :||:|    :|||::||||||:|: | |:|||| | |   | :|  || |||||: ||:
Db      37 HFGRLHCTTAVIRSINDQVLFVDKRNPPVFEDMPDIDRTANESQTRLIIYMYKDSEVRGL 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||:|||  ::| |||:||||||:|||||:|| | |||:|||| |||:|||| |
Db      97 AVTLSVKDGRMSTLSCKNKIISFEEMNPPENIDDIKSDLIFFQKRVPGH-NKMEFESSLY 155

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
           ||:||||:|| | |||:||::|| ||:|:|||: |
Db     156 EGHFLACQKEDDAFKLVLKRKDENGDKSVMFTLTN 190


RESULT 8
IL1A_PIG
ID   IL1A_PIG       STANDARD;      PRT;   270 AA.
AC   P18430;
DT   01-NOV-1990 (Rel. 16, Created)
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DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 alpha precursor (IL-1 alpha).
GN   IL1A.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=90332454; PubMed=2377484;
RA   Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA   Baker P.E.;
RT   "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL   Nucleic Acids Res. 18:4282-4282(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Huether M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52731; CAA36945.1; -.
DR   EMBL; M86730; AAA73198.1; -.
DR   PIR; S10532; S10532.
DR   HSSP; P01583; 1ITA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    112
FT   CHAIN       113    270       INTERLEUKIN-1 ALPHA.
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     89     89       N -> I (IN REF. 2).
FT   CONFLICT    242    242       F -> L (IN REF. 2).
FT   CONFLICT    255    255       P -> R (IN REF. 2).
SQ   SEQUENCE   270 AA;  30788 MW;  5677BF2B0EF63839 CRC64;

  Query Match             10.0%;  Score 81.5;  DB 1;  Length 270;
  Best Local Similarity   22.7%;  Pred. No. 1.3;
  Matches   30;  Conservative   32;  Mismatches   57;  Indels   13;  Gaps    6;

Qy       8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMAV 62
           | : :| :| | :  |  |: :  | :     :   :|    : | :: |  :    : |
Db     123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAAVLNNLDEAVKFDMAAYTSNDDSQLPV 182

Qy      63 TISVKCEKISXLSCEN--KIISFKEM-NPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSS 119
           |: :  |    :| :|  : :  ||:   |  |||  | : |:::    | |   |:|::
Db     183 TLRIS-ETRLFVSAQNEDEPVLLKELPETPKTIKDETSLLFFWEK----HGNMDYFKSAA 237

Qy     120 YEGYFLACEKER 131
           :   |:|  :|:
Db     238 HPKLFIATRQEK 249


RESULT 9
IL1A_RABIT
ID   IL1A_RABIT     STANDARD;      PRT;   267 AA.
AC   P04822;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 alpha precursor (IL-1 alpha).
GN   IL1A.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85297782; PubMed=2994016;
RA   Furutani Y., Notake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA   Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT   "Cloning and characterization of the cDNAs for human and rabbit
RT   interleukin-1 precursor.";
RL   Nucleic Acids Res. 13:5869-5882(1985).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X02852; CAA26605.1; -.
DR   PIR; B24073; B24073.
DR   HSSP; P01583; 1ITA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    112
FT   CHAIN       113    267       INTERLEUKIN-1 ALPHA.
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   267 AA;  30375 MW;  6D20533FD1FA4822 CRC64;

  Query Match             10.0%;  Score 81;  DB 1;  Length 267;
  Best Local Similarity   25.2%;  Pred. No. 1.4;
  Matches   32;  Conservative   27;  Mismatches   56;  Indels   12;  Gaps    5;

Qy      12 IRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTI-----FIISMYKDSQPRGMAVTISV 66
           :| :  :    |  |: |  | :|   |    : :     | : :|  |:   : ||: :
Db     127 LRIIKQEFTLNDALNQSLVRDTSDQYLRAAPLQNLGDAVKFDMGVYMTSEDSILPVTLRI 186
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Qy      67 KCEKISXLSCEN--KIISFKEM-NPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGY 123
           :  :| :|  : :  |||   |  | |::|||:||  :     ||  |:|::
Db     187 SQTPL-FVSAQNEDEPVLLKEMPETPRIITDSESDILFFWET---QGNKNYFKSAANPQL 242

Qy     124 FLACEKE 130
           |:| : |
Db     243 FIATKPE 249


RESULT 10
MUTL_CLOPE
ID   MUTL_CLOPE     STANDARD;      PRT;   674 AA.
AC   Q8XL86;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   DNA mismatch repair protein mutL.
GN   MUTL OR CPE1156.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / Type A;
RX   PubMed=11792842;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC   -!- FUNCTION: This protein is involved in the repair of mismatches in
CC       DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC       repair. May act as a "molecular matchmaker", a protein that
CC       promotes the formation of a stable complex between two or more
CC       DNA-binding proteins in an ATP-dependent manner without itself
CC       being part of a final effector complex (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AP003189; BAB80862.1; -.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR002099; DNA_mis_repair.
DR   InterPro; IPR004359; HIS_KIN_sig.
DR   InterPro; IPR002173; PfkB.
DR   TIGRFAMs; TIGR00585; mutl; 1.
DR   PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
KW   DNA repair; Complete proteome.
SQ   SEQUENCE   674 AA;  77205 MW;  2380566BB4500A3D CRC64;

  Query Match             9.5%;  Score 77.5;  DB 1;  Length 674;
  Best Local Similarity   25.9%;  Pred. No. 9;
  Matches   30;  Conservative   15;  Mismatches   40;  Indels   31;  Gaps    5;

Qy      17 DQVLFIDQGNRPLFE-------DMTDSDCR--------DNAPRTIFIISMYKDSQPRGMA 61
           :  |: |: |: :||       |  |:  |        |    |  | ||  : :  |
Db     547 EDYLYYDE-NKEIFEKAGFKISDFGDNSIRIEEVPYFLDKLNPTELITSMINNLKKMGTG 605

Qy      62 VTISVKCEKISXLSCE-----NKIISFKEM----------NPPDNIKDTKSDIIFF 102
           |: ||  ||: :||       | ::|  ||          | | :    :  || |
Db     606 ETVEVKYNKIASMSCRAAVKANDVLSILEMENLIEDLRYINDPFHCPHGRPTIIKF 661


RESULT 11
IL1A_HORSE
ID   IL1A_HORSE     STANDARD;      PRT;   270 AA.
AC   Q28385; O77743;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 alpha precursor (IL-1 alpha).
GN   IL1A.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96131982; PubMed=8578682;
RA   Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,
RA   Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL   Vet. Immunol. Immunopathol. 48:221-231(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285941; PubMed=9622738;
RA   Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT   "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
RT   and determination of their full-length cDNA sequences.";
RL   Am. J. Vet. Res. 59:704-711(1998).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D42146; BAA07717.1; -.
DR   EMBL; U92480; AAC39255.1; -.
DR   HSSP; P01583; 1ITA.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR003502; IL1_propep.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    112       BY SIMILARITY.
FT   CHAIN       113    270       INTERLEUKIN-1 ALPHA.
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    110    110       R -> K (IN REF. 2).
FT   CONFLICT    150    150       G -> V (IN REF. 2).
SQ   SEQUENCE   270 AA;  30806 MW;  381859713754DB90 CRC64;

  Query Match             9.4%;  Score 76.5;  DB 1;  Length 270;
  Best Local Similarity   22.3%;  Pred. No. 3.8;
  Matches   29;  Conservative   28;  Mismatches   62;  Indels   11;  Gaps    4;
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Qy       7 SKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTI-----FIISMYKDSQPRGMA 61
           :| : :| :| |    | |: : | :       |   :     | : |   :   :
Db     122 TKYNFMRIVNHQCTLNDALNQSVIRDTSGQYLATAALNNLDDAVKFDMGAYTSEEDSQLP 181

Qy      62 VTISV-KCEKISXLSCENKIISFKEM-NPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSS 119
           ||: : |         |:: :  ||| : |  |||  : : |::|    | :|  |:| :
Db     182 VTLRISKTRLFVSAQNEDEPVLLKEMPDTPKTIKDETNLLFFWER----HGSKNYFKSVA 237

Qy     120 YEGYFLACEK 129
           :   |:| ::
Db     238 HPKLFIATKQ 247


RESULT 12
OASB_MOUSE
ID   OASB_MOUSE     STANDARD;      PRT;   192 AA.
AC   Q60856;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)
DE   synthetase 1b) (2-5A synthetase 1B) (Fragment).
GN   OAS1B OR OIAS2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91232962; PubMed=1709495;
RA   Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;
RT   "The murine 2-5A synthetase locus: three distinct transcripts from two
RT   linked genes.";
RL   Nucleic Acids Res. 19:1917-1924(1991).
CC   -!- FUNCTION: THE 2-5A SYSTEM (THE OASS, 2-5A, AND RNASE L) MAY PLAY A
CC       ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
CC       GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC   -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
CC       into PPP(A2'P5'A)N oligomers, which activate the latent RNAse L
CC       that, when activated, cleaves single-stranded RNAs.
CC   -!- INDUCTION: BY INTERFERONS.
CC   -!- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X55982; CAA39455.1; -.
DR   MGD; MGI:97430; Oas1b.
DR   InterPro; IPR001797; 25A_synth.
DR   InterPro; IPR001201; PAP_25A_core.
DR   PROSITE; PS00832; 25A_SYNTH_1; PARTIAL.
DR   PROSITE; PS00833; 25A_SYNTH_2; PARTIAL.
DR   PROSITE; PS50152; 25A_SYNTH_3; 1.
KW   RNA-binding; Transferase; Nucleotidyltransferase;
KW   Interferon induction.
FT   NON_TER       1      1
FT   NON_TER     192    192
SQ   SEQUENCE   192 AA;  21936 MW;  4E1C011EF9024F46 CRC64;

  Query Match             9.3%;  Score 75.5;  DB 1;  Length 192;
  Best Local Similarity   23.2%;  Pred. No. 3.2;
  Matches   42;  Conservative   24;  Mismatches   50;  Indels   65;  Gaps    9;

Qy       3 GKLESKLSVIRN--------LNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKD 54
           |: :: | |  |        || | : | :  : | |   :  |
Db      11 GRSDADLVVFLNNLTSFEDQLNQQGVLIKEIKKQLCEVQHERRC---------------- 54

Qy      55 SQPRGMAVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDII-------------- 100
                    || |  |  |  :: :||| :: || :|: | |::
Db      55 ----------GVKFEVHSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLLDHLNILKK 103

Qy     101 ----FFQR---SVP-GHDNKMQFESSSYEGYFLACE--KERDLFKLI-----LKKEDELG 145
               |:      || | :  |:       : ||| |   | : | :|:     | || :||
Db     104 PNQQFYANLISGVPAGKEGKLSICFMGLQKYFLNCRPTKLKRLIRLVTHWYQLCKE-KLG 162

Qy     146 D 146
           |
Db     163 D 163


RESULT 13
Y414_MYCGE
ID   Y414_MYCGE     STANDARD;      PRT;  1036 AA.
AC   P47653; P47654; Q49457;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update),
DE   Hypothetical protein MG414.
GN   MG414.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
RN   [2]
RP   SEQUENCE OF 52-146 AND 733-833 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=94075230; PubMed=8253680;
RA   Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A survey of the Mycoplasma genitalium genome by using random
RT   sequencing.";
RL   J. Bacteriol. 175:7918-7930(1993).
CC   -!- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U39723; AAC71641.1; -.
DR   EMBL; U01695; AAB01008.1; -.
DR   EMBL; U01804; AAD12330.1; -.
DR   TIGR; MG414; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     24       POTENTIAL.
FT   TRANSMEM   1004   1024       POTENTIAL.
FT   CONFLICT    733    736       LEPT -> SRAS (IN REF. 2).
SQ   SEQUENCE   1036 AA;  123179 MW;  12A21F00F686A141 CRC64;

  Query Match             9.3%;  Score 75.5;  DB 1;  Length 1036;
  Best Local Similarity   21.9%;  Pred. No. 23;
  Matches   33;  Conservative   32;  Mismatches   65;  Indels   21;  Gaps    6;

Qy      14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEK- 70
           :|||: | :|: |  | |    |  : | |       | : ::     :   : |: :|
Db     845 SLNDEQLLVDKLNITLSEKRLQTTKNVRFNLKNKFINIHLVENKNQFNLVFDVDVRSKKL 904

Qy      71 -ISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEK 129
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          |  :: :|:: |        ::| | :  :       | || : |: :|        |
Db    905 FIKGVNNDNQVFSISY-----DLKITNNQTLLIV-DANGFDNSIWFDITS--------EN 950

Qy    130 ERDLFKLI---LKKEDELGDRSIMFTVQNED 157
          :  ||| :   ||: :    |   | ::::|
Db    951 QTQLFKALSFYLKQNNLQFKRVPDFNLKSQD 981


RESULT 14
CO3_MOUSE
ID   CO3_MOUSE      STANDARD;      PRT;  1663 AA.
AC   P01027;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Complement C3 precursor (HSE-MSF) [Contains: C3A anaphylatoxin].
GN   C3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=85038854; PubMed=6208565;
RA   Fey G.H., Lundwall A., Wetsel R.A., Tack B.F., de Bruijn M.H.L.,
RA   Domdey H.;
RT   "Nucleotide sequence of complementary DNA and derived amino acid
RT   sequence of murine complement protein C3.";
RL   Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
RN   [2]
RP   SEQUENCE OF 671-1663 FROM N.A. (LONG ISOFORM).
RX   MEDLINE=85054819; PubMed=6094532;
RA   Wetsel R.A., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H.;
RT   "Structure of murine complement component C3. II. Nucleotide sequence
RT   of cloned complementary DNA coding for the alpha chain.";
RL   J. Biol. Chem. 259:13857-13862(1984).
RN   [3]
RP   SEQUENCE OF 671-748 FROM N.A.
RX   MEDLINE=83117730; PubMed=6961437;
RA   Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
RT   "Characterization of the mRNA and cloned cDNA specifying the third
RT   component of mouse complement.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
RN   [4]
RP   SEQUENCE OF 658-761 FROM N.A.
RX   MEDLINE=84201365; PubMed=6609661;
RA   Fey G.H., Wiebauer K., Domdey H.;
RT   "Amino acid sequences of mouse complement C3 derived from nucleotide
RT   sequences of cloned cDNA.";
RL   Ann. N.Y. Acad. Sci. 421:307-312(1983).
RN   [5]
RP   SEQUENCE OF 1-34 FROM N.A.
RX   MEDLINE=83117622; PubMed=6985486;
RA   Wiebauer K., Domdey H., Diggelmann H., Fey G.;
RT   "Isolation and analysis of genomic DNA clones encoding the third
RT   component of mouse complement.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
RN   [6]
RP   SEQUENCE OF 25-41 AND 749-760.
RX   MEDLINE=93373334; PubMed=8364938;
RA   Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
RT   "A paracrine migration-stimulating factor for metastatic tumor cells
RT   secreted by mouse hepatic sinusoidal endothelial cells:
RT   identification as complement component C3b.";
RL   Cancer Res. 53:4418-4423(1993).
RN   [7]
RP   ALTERNATIVE INITIATION.
RX   MEDLINE=95053742; PubMed=7964485;
RA   Cahen-Kramer Y., Martensson I.L., Melchers F.;
RT   "The structure of an alternate form of complement C3 that displays
RT   costimulatory growth factor activity for B lymphocytes.";
RL   J. Exp. Med. 180:2079-2088(1994).
CC   -!- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
CC       COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
CC       REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
CC       AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
CC       THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
CC   -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
CC       C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC       INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC       PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC       BASOPHILIC LEUKOCYTES. THE SHORT ISOFORM HAS B-CELL STIMULATORY
CC       ACTIVITY.
CC   -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC       residues, forming two chains, beta and alpha, linked by a
CC       disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC       chain, releasing C3A anaphylatoxin and generating C3B (beta chain
CC       + alpha' chain).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC       short form; are produced by alternative initiation.
CC   -!- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR I
CC       AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS
CC       RELEASED.
CC   -!- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I)
CC       TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH
CC       AS C3D OR C3G.
CC   -!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
CC   -!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; K02782; AAC42013.1; -.
DR   EMBL; J00369; AAA37336.1; -.
DR   EMBL; J00367; AAA37336.1; JOINED.
DR   EMBL; M33032; AAA37378.1; -.
DR   EMBL; Z37998; CAA86099.2; -.
DR   PIR; A05290; C3MS.
DR   HSSP; P01024; 1C3D.
DR   MGD; MGI:88227; C3.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacrogloblnA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF01759; NTR; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   SMART; SM00104; ANATO; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW   Complement pathway; Complement alternate pathway; Plasma;
KW   Inflammatory response; Glycoprotein; Signal; Alternative initiation.
FT   SIGNAL        1     24
FT   CHAIN        25   1663       COMPLEMENT C3.
FT   CHAIN        25    666       COMPLEMENT C3, BETA CHAIN.
FT   CHAIN       671   1663       COMPLEMENT C3, ALPHA CHAIN.
FT   CHAIN      1129   1663       COMPLEMENT C3, SHORT ISOFORM.
FT   INIT_MET   1129   1129       FOR SHORT ISOFORM.
FT   PEPTIDE     671    748       C3A ANAPHYLATOXIN.
FT   CHAIN       749   1663       C3B (ALPHA' CHAIN).
FT   PEPTIDE     749    954       C3C FRAGMENT.
FT   PEPTIDE     955   1303       C3DG FRAGMENT.
FT   PEPTIDE     955   1001       C3G FRAGMENT.
FT   PEPTIDE    1002   1303       C3D FRAGMENT.
FT   PEPTIDE    1304   1320       C3F FRAGMENT.
FT   SITE        748    749       CLEAVAGE (BY C3 CONVERTASE).
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FT   SITE       1303   1304       CLEAVAGE (BY FACTOR I).
FT   SITE       1320   1321       CLEAVAGE (BY FACTOR I).
FT   DOMAIN      693    728       ANAPHYLATOXIN-LIKE.
FT   DISULFID    559    816       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    626    661       BY SIMILARITY.
FT   DISULFID    693    720       BY SIMILARITY.
FT   DISULFID    694    727       BY SIMILARITY.
FT   DISULFID    707    728       BY SIMILARITY.
FT   DISULFID    873   1513       BY SIMILARITY.
FT   DISULFID   1101   1158       BY SIMILARITY.
FT   DISULFID   1358   1489       BY SIMILARITY.
FT   DISULFID   1389   1458       BY SIMILARITY.
FT   DISULFID   1506   1511       BY SIMILARITY.
FT   DISULFID   1518   1590       BY SIMILARITY.
FT   DISULFID   1537   1661       BY SIMILARITY.
FT   DISULFID   1637   1646       BY SIMILARITY.
FT   CARBOHYD    939    939       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   1617   1617       N-LINKED (GLCNAC. . .).
FT   THIOLEST   1010   1013       BY SIMILARITY.
SQ   SEQUENCE   1663 AA;  186482 MW;  DE5546CC769BEA19 CRC64;

  Query Match             9.3%;  Score 75.5;  DB 1;  Length 1663;
  Best Local Similarity   23.1%;  Pred. No. 40;
  Matches   25;  Conservative   23;  Mismatches   45;  Indels   15;  Gaps    4;

Qy      18 QVLFIDQGN--RPLFEDMTDSDCRDNAPRT----IFIISMYKDSQPRGMAVTISVKCEKI 71
           :|| : ||:  : | :|   :    | | :       :   ||: |     | :::
Db     387 KVLVVTQGSNAKALTQDDGVAKLSINTPNSRQPLTITVRTKKDTLPESRQATKTMEAHPY 446

Qy      72 SXLSCENKI----ISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQF 115
           | :   |      :|  |: | ||:     :: |  |: |||: |:::
Db     447 STMHNSNNYLHLSVSRMELKPGDNL-----NVNFHLRTDPGHEAKIRY 489


RESULT 15
ECM_HUMAN
ID   ECM_HUMAN      STANDARD;      PRT;  1228 AA.
AC   Q13201;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelial cell multimerin precursor.
GN   MMRN OR ECM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 368-376.
RC   TISSUE=Endothelial cells;
RX   MEDLINE=95355440; PubMed=7629143;
RA   Hayward C.P.M., Hassell J.A., Denomme G.A., Rachubinski R.A.,
RA   Brown C., Kelton J.G.;
RT   "The cDNA sequence of human endothelial cell multimerin. A unique
RT   protein with RGDS, coiled-coil, and epidermal growth factor-like
RT   domains and a carboxyl terminus similar to the globular domain of
RT   complement C1q and collagens type VIII and X.";
RL   J. Biol. Chem. 270:18246-18251(1995).
CC   -!- FUNCTION: CARRIER PROTEIN FOR PLATELET (BUT NOT PLASMA) FACTOR
CC       V/VA. MAY PLAY A ROLE IN THE STORAGE AND STABILIZATION OF FACTOR V
CC       IN PLATELETS.
CC   -!- SUBUNIT: MULTIMERIC. COMPOSED OF VARYING SIZED, DISULFIDE-LINKED
CC       MULTIMERS, THE SMALLEST OF WHICH IS A HOMOTRIMER. PROTEOLYSIS OF
CC       THE PROMULTIMERIN IN THE N-TERMINAL REGION, LEADS TO THE MATURE
CC       P155 FORM THAT IS STORED IN PLATELETS.
CC   -!- TISSUE SPECIFICITY: SYNTHESIZED BY ENDOTHELIAL CELLS AND
CC       MEGAKARYOCYTES. STORED IN PLATELET ALPHA GRANULES AND ENDOTHELIAL
CC       CELL WEIBEL-PALADE BODIES, FOLLOWING ACTIVATION OF THESE CELLS, IT
CC       IS RELEASED AND ATTACHED TO MEGAKARYOCYTES, PLATELETS, ENDOTHELIUM
CC       AND SUBENDOTHELIUM OF BLOOD VESSELS. NOT FOUND IN PLASMA. FOUND IN
CC       VASCULAR TISSUES SUCH AS PLACENTA, LUNG, AND LIVER.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- PTM: EXTENSIVELY N-GLYCOSYLATED.
CC   -!- DISEASE: DEFICIENCY IN MULTIMERIN DUE TO PROTEOLYTIC DEGRADATION
CC       WITHIN THE PLATELET ALPHA GRANULES IS ASSOCIATED WITH AN AUTOSOMAL
CC       DOMINANT BLEEDING DISORDER (FACTOR V QUEBEC).
CC   -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U27109; AAC52065.1; -.
DR   Genew; HGNC:7178; MMRN.
DR   MIM; 601456; -.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00386; C1q; 1.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   SMART; SM00110; C1Q; 1.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS01113; C1Q; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
KW   Signal; Glycoprotein; EGF-like domain; Coiled coil.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   1228       ENDOTHELIAL CELL MULTIMERIN.
FT   DOMAIN     1041   1077       EGF-LIKE.
FT   DOMAIN     1119   1149       C1Q.
FT   DOMAIN      333    365       COILED COIL (POTENTIAL).
FT   DOMAIN      400    430       COILED COIL (POTENTIAL).
FT   DOMAIN      503    523       COILED COIL (POTENTIAL).
FT   DOMAIN      580    650       COILED COIL (POTENTIAL).
FT   DOMAIN      675    726       COILED COIL (POTENTIAL).
FT   DOMAIN      819    869       COILED COIL (POTENTIAL).
FT   DOMAIN      189    192       POLY-SER.
FT   DOMAIN      309    313       POLY-GLN.
FT   SITE        186    188       CELL ATTACHMENT SITE (POTENTIAL).
FT   DISULFID   1045   1056       BY SIMILARITY.
FT   DISULFID   1050   1065       BY SIMILARITY.
FT   DISULFID   1067   1076       BY SIMILARITY.
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    120    120       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    344    344       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    431    431       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    507    507       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    541    541       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    576    576       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    618    618       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    680    680       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    729    729       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    783    783       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    828    828       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    840    840       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    921    921       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    933    933       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    942    942       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    981    981       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1020   1020       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1075   1075       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1228 AA;  138071 MW;  EAA98B0A17E2C4CD CRC64;

  Query Match             9.2%;  Score 74.5;  DB 1;  Length 1228;
  Best Local Similarity   21.3%;  Pred. No. 35;
  Matches   32;  Conservative   36;  Mismatches   47;  Indels   35;  Gaps    9;
```

```
Qy       1 YFGKLESKLSVIRNLNDQVL----FIDQGNRPLFEDMTD------SDCRDNAPR-TIFII 49
           |:  |   || :: :::|:|      || | |  | :::      |   :|  : :: ::
Db     502 YYESLNKTLSKLKEVHEQLLSTEQVSDQKNAPAAESVSNNVTEYMSTLHENIKKQSLMML 561

Qy      50 SMYKD---SQPRGMAVTISVKCEKISXL-SCENKI------ISFKEMNPPDN---IKDTK 96
           |::|    : :   :|:|:: || |    ||: :        |:  :  :|   :  |
Db     562 QMFEDLHIQESKINNLTVSLEMEKESLRGECEDMLSKCRNDFKFQLKDTEENLHVLNQTL 621

Qy      97 SDIIFFQRSVPGHDNKM-----QFESSSYE 121
           ::::|        ||||     |    :|:
Db     622 AEVLF------PMDNKMDKMSEQLNDLTYD 645


Search completed: April  4, 2003, 10:59:50
Job time : 14 secs
```

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:57:21 ; Search time 85 Seconds
(without alignments)
380.581 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	798	98.3	193	4	Q96KJ8	Q96kj8 homo sapien
2	792	97.5	193	6	Q9BGI5	Q9bgi5 macaca mula
3	654	80.5	178	6	Q9MZL8	Q9mzl8 bos taurus
4	648	79.8	193	6	Q9GL09	Q9gl09 ovis aries
5	634	78.1	192	6	Q95M33	Q95m33 felis silve
6	626	77.1	192	6	Q9N1P7	Q9n1p7 sus scrofa
7	441	54.3	196	11	Q91Z66	Q91z66 sigmodon hi
8	313	38.5	84	6	Q95LE7	Q95le7 canis famil
9	204	25.1	45	4	Q9NQ49	Q9nq49 homo sapien
10	193	23.8	211	13	Q98SQ1	Q98sq1 anas platyr
11	182.5	22.5	198	13	Q9I8D2	Q9i8d2 gallus gall
12	178.5	22.0	196	13	Q8QFQ8	Q8qfq8 gallus gall
13	88	10.8	4643	5	Q9VW71	Q9vw71 drosophila
14	85	10.5	381	3	O43031	O43031 schizosacch
15	82	10.1	263	3	O74316	O74316 schizosacch
16	82	10.1	1501	5	Q22699	Q22699 caenorhabdi
17	81.5	10.0	617	5	Q25986	Q25986 plasmodium
18	81.5	10.0	1049	2	Q93KF0	Q93kf0 caldicellul
19	80.5	9.9	866	16	O84500	O84500 chlamydia t
20	80	9.9	1449	16	Q8XJR3	Q8xjr3 clostridium
21	79.5	9.8	595	10	Q9SDM4	Q9sdm4 dunaliella
22	79.5	9.8	1044	3	O94173	O94173 pneumocysti
23	79	9.7	452	16	O25249	O25249 helicobacte
24	78.5	9.7	204	2	Q9ZNJ7	Q9znj7 clostridium
25	78	9.6	473	5	O16673	O16673 caenorhabdi
26	77.5	9.5	1251	13	Q91365	Q91365 coturnix co
27	77	9.5	364	16	Q9PM33	Q9pm33 campylobact
28	76.5	9.4	454	6	Q9BGD1	Q9bgd1 micronycter
29	76.5	9.4	840	12	Q9QBA2	Q9qba2 yaba monkey
30	76.5	9.4	2383	10	Q8S484	Q8s484 zea mays (m
31	76	9.4	632	10	O80569	O80569 arabidopsis
32	76	9.4	632	10	Q8RY34	Q8ry34 arabidopsis
33	76	9.4	747	10	O82393	O82393 arabidopsis
34	76	9.4	847	4	Q9NUC1	Q9nuc1 homo sapien
35	76	9.4	1093	16	Q8XK91	Q8xk91 clostridium
36	75.5	9.3	137	5	O77077	O77077 plasmodium
37	75.5	9.3	251	11	Q8VI98	Q8vi98 mus musculu
38	75.5	9.3	331	5	Q8SVZ4	Q8svz4 encephalito
39	75.5	9.3	454	6	Q9BGE4	Q9bge4 erophylla s
40	75.5	9.3	454	6	Q9BGA8	Q9bga8 sturnira li
41	75	9.2	536	17	Q8U2P1	Q8u2p1 pyrococcus
42	75	9.2	1064	13	Q90601	Q90601 gallus gall
43	75	9.2	1247	5	Q95QV2	Q95qv2 caenorhabdi
44	75	9.2	2470	13	Q90681	Q90681 gallus gall
45	74.5	9.2	334	10	Q9ZSB9	Q9zsb9 arabidopsis

ALIGNMENTS

RESULT 1
Q96KJ8
ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF380360; AAK57024.1; -.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 4; Length 193;
Best Local Similarity 97.5%; Pred. No. 1.2e-71;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db      37 YFGKLESKLSVIRNLNNQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           |||||||||||| |||||||||||:||||||||||||||||||||||||||||||||||||
Db      97 AVTISVKCEKISTLSCENKIISFKEVNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           ||||| |||||||||||||||||||||||||||||||
Db     157 EGYFLTCEKERDLFKLILKKEDELGDRSIMFTVQNED 193
```

RESULT 2
Q9BGI5

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ID   Q9BGI5      PRELIMINARY;      PRT;   193 AA.
AC   Q9BGI5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Interleukin-18.
GN   IL18.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21229850; PubMed=11331040;
RA   Giavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA   Hodara V.L.;
RT   "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT   Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT   Replication.";
RL   J. Interferon Cytokine Res. 21:173-180(2001).
DR   EMBL; AF303732; AAK13416.1; -.
SQ   SEQUENCE   193 AA;  22325 MW;  B2BD29C033BB0B5E CRC64;

  Query Match             97.5%;  Score 792;  DB 6;  Length 193;
  Best Local Similarity   95.5%;  Pred. No. 4.8e-71;
  Matches  150;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           ||||||||||:||||||||||||||||||||||||||||||||||||:||||||||||
Db      37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINMYKDSQPRGM 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           || |||||||| |||||:|||||||||||||||||||||||||||||||||||||||||||
Db      97 AVAISVKCEKISTLSCENRIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           |||||||||||||:||||||:||||||||||||||||
Db     157 EGYFLACEKERDLYKLILKKKDELGDRSIMFTVQNED 193


RESULT 3
Q9MZL8
ID   Q9MZL8      PRELIMINARY;      PRT;   178 AA.
AC   Q9MZL8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Interleukin-18 (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY, LIVER, AND BLOOD;
RA   Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT   "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT   characterization of the biologic activities of the recombinant
RT   cytokine.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF173175; AAF89833.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
FT   NON_TER       1      1
FT   NON_TER     178    178
SQ   SEQUENCE   178 AA;  20631 MW;  816D6B2B88ACB497 CRC64;

  Query Match             80.5%;  Score 654;  DB 6;  Length 178;
  Best Local Similarity   77.1%;  Pred. No. 2.3e-57;
  Matches  121;  Conservative   23;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           :||||| |||:||||||||||||:|||:|:|||| |||| ||||:||||| ||||| ||:
Db      22 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSDNAPQTIFIIYMYKDSLTRGL 81

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||:|:|:| |||||||:|||||||||| : :|||||||||||||:|:||||| |
Db      82 AVTISVQCKKMSTLSCENKIVSFKEMNPPDNIDNEESDIIFFQRSVPGHDDKIQFESSLY 141

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :|||||||:|| |||||||||:|:  |:|:|||||||::
Db     142 KGYFLACKKENDLFKLILKKQDDNRDKSVMFTVQNQN 178


RESULT 4
Q9GL09
ID   Q9GL09      PRELIMINARY;      PRT;   193 AA.
AC   Q9GL09;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Interleukin-18 (IGIF).
GN   IL-18.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT   "Cloning of Ovine interleukin 18 cDNA.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ401033; CAC09326.2; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   193 AA;  22166 MW;  CCD0A329062EF18C CRC64;

  Query Match             79.8%;  Score 648;  DB 6;  Length 193;
  Best Local Similarity   77.7%;  Pred. No. 1e-56;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           :||||| |||:||||||||||| |||:|:|||| |||| ||||:||||| ||||  ||:
Db      37 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSDCSDNAPQTIFIIYMYKDSLTRGL 96

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||:|:|:| |||||||||||||||||| :  |||||||||||||:|:||||| |
Db      97 AVTISVQCKKMSTLSCENKIISFKEMNPPDNIDNEGSDIIFFQRSVPGHDDKIQFESSLY 156

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :|||||||:|| |||||||::|:  |:|||||||::
Db     157 KGYFLACKKENDLFKLILKRQDDNRDKSIMFTVQNKN 193


RESULT 5
Q95M33
ID   Q95M33      PRELIMINARY;      PRT;   192 AA.
AC   Q95M33;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interferon-gamma inducing factor.
GN   IGIF.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
RT   "Nucleotide sequence of feline IGIF cDNA (provisional).";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y13923; CAC42918.1; -.
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SQ   SEQUENCE   192 AA;  22068 MW;  5878C3DAC7A43358 CRC64;

  Query Match             78.1%;  Score 634;  DB 6;  Length 192;
  Best Local Similarity   76.4%;  Pred. No. 2.5e-55;
  Matches  120;  Conservative   21;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||| |||::|||||||||||:||::|:|||| |||| |||||| ||| |||||  ||:
Db      36 YFGKLEHKLSILRNLNDQVLFINQGDQPVFEDMPDSDCTDNAPRTEFIIYMYKDSLTRGL 95

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||  : :| ||||||||||||||:||::| |  :|||||||||||||:|:||||| |
Db      96 AVTISVNYKTMSTLSCENKIISFKEMSPPESINDEGNDIIFFQRSVPGHDDKIQFESSLY 155

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :|||||||||:|||||||||:|| ||:||||||||::
Db     156 KGYFLACEKEKDLFKLILKKKDENGDKSIMFTVQNKN 192


RESULT 6
Q9N1P7
ID   Q9N1P7      PRELIMINARY;      PRT;   192 AA.
AC   Q9N1P7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-18.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RX   MEDLINE=20356335; PubMed=10901174;
RA   Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
RT   "Cloning, sequencing, and expression of porcine interleukin-18 in
RT   Escherichia coli.";
RL   Mol. Cells 10:343-347(2000).
DR   EMBL; AF176949; AAF35169.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   192 AA;  21969 MW;  A51EB7A4E221A16D CRC64;

  Query Match             77.1%;  Score 626;  DB 6;  Length 192;
  Best Local Similarity   73.9%;  Pred. No. 1.5e-54;
  Matches  116;  Conservative   25;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||| |||:|||||||||||:||:: :|||| |||| ||||:|:|||  |||||  ||:
Db      36 YFGKLEPKLSIIRNLNDQVLFINQGHQAVFEDMPDSDCSDNAPQTVFIIYMYKDSLTRGL 95

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           ||||||:|:|:| |||:|| :|||||:||||| |  :|||||||||||||:|:||||| |
Db      96 AVTISVQCKKMSTLSCKNKTLSFKEMSPPDNIDDEGNDIIFFQRSVPGHDDKIQFESSLY 155

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
           :||||||:|| |||||||::|| ||:|| ||||:::
Db     156 KGYFLACKKENDLFKLILKEKDECGDKSITFTVQSKN 192


RESULT 7
Q91Z66
ID   Q91Z66      PRELIMINARY;      PRT;   196 AA.
AC   Q91Z66;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 18.
GN   IL18.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY059406; AAL26703.1; -.
SQ   SEQUENCE   196 AA;  22545 MW;  E27C5BDC397F951C CRC64;

  Query Match             54.3%;  Score 441;  DB 11;  Length 196;
  Best Local Similarity   59.4%;  Pred. No. 4e-36;
  Matches   92;  Conservative   24;  Mismatches   37;  Indels    2;  Gaps    2;

Qy       2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYK-DSQPRGM 60
           | |  |  :||||:|| |||||:   |:|||| |:| : |  :|  || ||| |  | |:
Db      39 FFKESSTTAVIRNMNDYVLFIDREKSPVFEDMPDADQKANEAQTRLIIYMYKTDFNPGGL 98

Qy      61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
             ||:||:   :  |||:|:||||:||:||  |  ||||:|||||:|||| |||:|||| :
Db      99 PVTLSVRDRTMRTLSCKNQIISFEEMDPPLEIDGTKSDLIFFQRAVPGH-NKMKFESSLH 157

Qy     121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
           ||:||||||:: | |||||||:||  | ||:||| |
Db     158 EGHFLACERDGDSFKLILKKKDENWDTSIIFTVTN 192


RESULT 8
Q95LE7
ID   Q95LE7      PRELIMINARY;      PRT;    84 AA.
AC   Q95LE7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IL-18 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RA   Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT   "Semi-quantification of canine cytokine expression by one tube RT-
RT   PCR.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF327900; AAL26920.1; -.
FT   NON_TER       1      1
FT   NON_TER      84     84
SQ   SEQUENCE   84 AA;  9568 MW;  19BD9E27F336774B CRC64;

  Query Match             38.5%;  Score 313;  DB 6;  Length 84;
  Best Local Similarity   74.7%;  Pred. No. 8.3e-24;
  Matches   59;  Conservative   10;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
           |||||| |||:|||||||||||:::||:|:|||| |||| |||| ||||| |||||  ||:
Db       5 YFGKLEPKLSIIRNLNDQVLFVNEGNQPVFEDMPDSDCTDNAPHTIFIIYMYKDSLTRGL 64

Qy      61 AVTISVKCEKISXLSCENK 79
           ||||||| : :| |||:||
Db      65 AVTISVKYKTMSTLSCKNK 83


RESULT 9
Q9NQ49
ID   Q9NQ49      PRELIMINARY;      PRT;    45 AA.
AC   Q9NQ49;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Interleukin-18 (Fragment).
GN   IL-18.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Farhan A.J., Pravica V., Hutchinson I.V.;
RT   "Identification of Human Intreleukin-18 gene polymorphisms.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ295724; CAC01436.1; -.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5266 MW;  DF3A626507E3D61A CRC64;

  Query Match             25.1%;  Score 204;  DB 4;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-13;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 39
           |||||||||||||||||||||||||||||||||||||||
Db       7 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 45


RESULT 10
Q98SQ1
ID   Q98SQ1      PRELIMINARY;      PRT;   211 AA.
AC   Q98SQ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Interleukin-18 (Fragment).
GN   IL-18.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT   "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF336122; AAK26322.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   211 AA;  24541 MW;  CA6FC63538211B2B CRC64;

  Query Match             23.8%;  Score 193;  DB 13;  Length 211;
  Best Local Similarity   36.5%;  Pred. No. 2e-11;
  Matches   61;  Conservative   29;  Mismatches   63;  Indels   14;  Gaps    9;

Qy       2 FGKLESKLSVIRNLNDQVLFIDQG-NRPLFEDMTDSDCRDNAPRTIFIISMYKDSQP-RG 59
           | | ::    :||:| ||| :    |   |||:|| : : :    | : || : |  |
Db      43 FSKEKTLHRFLRNVNSQVLVVRPDLNMAAFEDVTDQEMKSGSGMN-FCMHCYKTTTPSAG 101

Qy      60 MAVTISVKCE-KISXLSCENK----IISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNK-M 113
           | |  ||: | |   : || :    |: |:|   | :|   :|:||||:::   : :|
Db     102 MPVAFSVRVEDKSYYMCCEEEHGKMIVRFREGEVPKDIPG-ESNIIFFKKTFTSYSSKAF 160

Qy     114 QFESSSYEGYFLACEKERDLFKLILKK---EDELGDRS-IMFTVQNE 156
           :|| |   | ||| |:|  | ||||||   |||: : : |  |  ||
Db     161 KFEYSLERGMFLAFEEEDSLRKLILKKLPREDEVDETTKITLTSHNE 207


RESULT 11
Q9I8D2
ID   Q9I8D2      PRELIMINARY;      PRT;   198 AA.
AC   Q9I8D2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 18.
GN   IL-18.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20508574; PubMed=11054275;
RA   Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA   Kaspers B., Weining K.C.;
RT   "cDNA cloning of biologically active chicken Interleukin-18.";
RL   J. Interferon Cytokine Res. 20:879-883(2000).
DR   EMBL; AJ277865; CAB96214.1; -.
FT   CHAIN        30    198       INTERLEUKIN 18.
SQ   SEQUENCE   198 AA;  22918 MW;  29BB77DC3E3C6600 CRC64;

  Query Match             22.5%;  Score 182.5;  DB 13;  Length 198;
  Best Local Similarity   36.8%;  Pred. No. 2.1e-10;
  Matches   57;  Conservative   25;  Mismatches   60;  Indels   13;  Gaps    7;

Qy      13 RNLNDQVLFIDQG-NRPLFEDMTDSDCRDNAPRTIFIISMYKDSQP-RGMAVTISVKCEK 70
           ||:| |:| :    |   |||:|| : :  :    | |  || : |  || | ||: |
Db      42 RNVNSQLLVVRPDLNVAAFEDVTDQEVKSGS-GMYFDIHCYKTTAPSAGMPVAFSVQVED 100

Qy      71 ISXLSCENK-----IISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNK-MQFESSSYEGYF 124
           |   |  |     :: |:|   | :|   :|:||||:::     :|  :|| |  :| |
Db     101 KSYYMCCEKEHGKMVVRFREGEVPKDIPG-ESNIIFFKKTFTSCSSKAFKFEYSLEQGMF 159

Qy     125 LACEKERDLFKLILKK---EDELGDRSIMFTVQNE 156
           || |:|  | ||||||   |||: : :   |  ||
Db     160 LAFEEEDSLRKLILKKLPREDEVDETTKFVTSHNE 194


RESULT 12
Q8QFQ8
ID   Q8QFQ8      PRELIMINARY;      PRT;   196 AA.
AC   Q8QFQ8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-18 precursor.
GN   IL18.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rothwell L., Buerstedde J.M., Kaiser P.;
RT   "Cloning and characterisation of chicken interleukin-18.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ276025; CAC81652.1; -.
KW   Signal.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    196       INTERLEUKIN-18.
SQ   SEQUENCE   196 AA;  22787 MW;  4947DECECCB92414 CRC64;

  Query Match             22.0%;  Score 178.5;  DB 13;  Length 196;
  Best Local Similarity   34.3%;  Pred. No. 5.1e-10;
  Matches   60;  Conservative   26;  Mismatches   68;  Indels   21;  Gaps    8;

Qy       1 YFGKLESKL--------SVIRNLNDQVLFIDQG-NRPLFEDMTDSDCRDNAPRTIFIISM 51
           || :||              ||:| |:| :    |   |||:|| : :  :    | |
Db      20 YFEELECDAFCKDKTIKRFFRNVNSQLLVVRPDLNVAAFEDVTDQEVKSGS-GMYFDIHC 78

Qy      52 YKDSQPRG-MAVTISVKCEKISXLSCENK----IISFKEMNPPDNIKDTKSDIIFFQRS 105
           || : |   | |  ||: |  |   |  |     :: |:|   | :|   :|:||||::
Db      79 YKTTAPSARMPVAFSVQVEDKSYYMCCEKEHGKMVVRFREGEVPKDIPG-ESNIIFFKKT 137

Qy     106 VPGHDNK-MQFESSSYEGYFLACEKERDLFKLILKK---EDELGDRSIMFTVQNE 156
               :|  :|| |  :| ||| |:|  | ||||||   |||: : :   |  ||
Db     138 FTSCSSKAFKFEYSLEQGMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSHNE 192
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RESULT 13
Q9VW71
ID   Q9VW71      PRELIMINARY;      PRT;  4643 AA.
AC   Q9VW71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative fat-like cadherin precursor (CG7749 protein).
GN   CG7749.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- FUNCTION: MAY BE INVOLVED IN CELL ADHESION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
DR   EMBL; AE003515; AAF49078.1; -.
DR   HSSP; P15116; 1NCI.
DR   FlyBase; FBgn0036930; fat2.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR002126; Cadherin.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001791; Laminin_G.
DR   Pfam; PF00028; cadherin; 31.
DR   Pfam; PF00008; EGF; 5.
DR   Pfam; PF00054; laminin_G; 1.
DR   PRINTS; PR00205; CADHERIN.
DR   SMART; SM00112; CA; 33.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00001; EGF_like; 5.
DR   SMART; SM00282; LamG; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00232; CADHERIN_1; 17.
DR   PROSITE; PS50268; CADHERIN_2; 41.
DR   PROSITE; PS00022; EGF_1; 5.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01187; EGF_CA; 1.
KW   Hypothetical protein; Cell adhesion; Signal; Transmembrane; Repeat;
KW   EGF-like domain; Glycoprotein; Calcium-binding.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36   4643       PUTATIVE FAT-LIKE CADHERIN.
FT   DOMAIN       36   1647       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1648   1668       POTENTIAL.
FT   DOMAIN     1669   4643       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       68    180       CADHERIN 1.
FT   DOMAIN      189    288       CADHERIN 2.
FT   DOMAIN      293    397       CADHERIN 3.
FT   DOMAIN      406    504       CADHERIN 4.
FT   DOMAIN      513    610       CADHERIN 5.
FT   DOMAIN      619    713       CADHERIN 6.
FT   DOMAIN      778    874       CADHERIN 7.
FT   DOMAIN      883    977       CADHERIN 8.
FT   DOMAIN      986   1085       CADHERIN 9.
FT   DOMAIN     1094   1190       CADHERIN 10.
FT   DOMAIN     1199   1296       CADHERIN 11.
FT   DOMAIN     1305   1402       CADHERIN 12.
FT   DOMAIN     1413   1503       CADHERIN 13.
FT   DOMAIN     1512   1609       CADHERIN 14.
FT   DOMAIN     1618   1714       CADHERIN 15.
FT   DOMAIN     1723   1812       CADHERIN 16.
FT   DOMAIN     1821   1929       CADHERIN 17.
FT   DOMAIN     1948   2030       CADHERIN 18.
FT   DOMAIN     2024   2137       CADHERIN 19.
FT   DOMAIN     2146   2232       CADHERIN 20.
FT   DOMAIN     2247   2338       CADHERIN 21.
FT   DOMAIN     2347   2465       CADHERIN 22.
FT   DOMAIN     2474   2567       CADHERIN 23.
FT   DOMAIN     2576   2670       CADHERIN 24.
FT   DOMAIN     2679   2779       CADHERIN 25.
FT   DOMAIN     2788   2876       CADHERIN 26.
FT   DOMAIN     2885   2983       CADHERIN 27.
FT   DOMAIN     2992   3083       CADHERIN 28.
FT   DOMAIN     3092   3185       CADHERIN 29.
FT   DOMAIN     3194   3289       CADHERIN 30.
FT   DOMAIN     3298   3394       CADHERIN 31.
FT   DOMAIN     3403   3499       CADHERIN 32.
FT   DOMAIN     3508   3604       CADHERIN 33.
FT   DOMAIN     3618   3671       CADHERIN 34.
FT   DOMAIN     3819   3879       EGF-LIKE 1.
FT   DOMAIN     3881   3919       EGF-LIKE 2.
FT   DOMAIN     4129   4166       EGF-LIKE 3.
FT   DOMAIN     4168   4205       EGF-LIKE 4.
FT   DOMAIN     4243   4279       EGF-LIKE 5.
FT   DISULFID   3823   3835       POTENTIAL.
FT   DISULFID   3830   3867       POTENTIAL.
FT   DISULFID   3869   3878       POTENTIAL.
FT   DISULFID   3885   3896       POTENTIAL.
FT   DISULFID   3890   3907       POTENTIAL.
FT   DISULFID   3909   3918       POTENTIAL.
FT   DISULFID   4133   4144       POTENTIAL.
FT   DISULFID   4138   4154       POTENTIAL.
FT   DISULFID   4156   4165       POTENTIAL.
FT   DISULFID   4172   4183       POTENTIAL.
FT   DISULFID   4177   4193       POTENTIAL.
FT   DISULFID   4195   4204       POTENTIAL.
FT   DISULFID   4247   4258       POTENTIAL.
FT   DISULFID   4252   4267       POTENTIAL.
FT   DISULFID   4269   4278       POTENTIAL.
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FT   CARBOHYD     65     65       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    364    364       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    779    779       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    843    843       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    923    923       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1106   1106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1198   1198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1312   1312       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1439   1439       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1473   1473       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1511   1511       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   4643 AA;  517614 MW;  7EC52BD36ADD4E89 CRC64;

  Query Match             10.8%;  Score 88;  DB 5;  Length 4643;
  Best Local Similarity   23.6%;  Pred. No. 18;
  Matches   38;  Conservative   25;  Mismatches   56;  Indels   42;  Gaps    7;

Qy      32 DMTDSDCRDNAPRTIFIISMY----KDSQPRGMAVTISVKCEKISXLSCENKIISF--KE 85
           |::  |  || |  :|:   |        |:|   || :: : |   | ||  : :  |:
Db    2124 DISVLDVNDNCP--LFVNMPYYATVSIDDPKG---TIIMQVKAIDLDSAENGEVRYELKK 2178

Qy      86 MNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL------------ 133
             |      | ||  :  :: | ||:   :   ::|:|    |  |  |
Db    2179 GNGELFKLDRKSGELSIKQHVEGHNRNYELTVAAYDGAITPCSSEAPLQVKVIDRSMPVF 2238

Qy     134 ---FKLILKKED--------------ELGDRSIMFTVQNE 156
              |  :  |||                || ||:::|: :|
Db    2239 EKQFYTVSVKEDVEMYSALSVSIEAESPLG-RSLIYTISSE 2278


RESULT 14
O43031
ID   O43031      PRELIMINARY;      PRT;   381 AA.
AC   O43031; Q9US93;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Hypothetical 44.2 kDa protein C3B9.02C in chromosome II.
GN   SPBC3B9.02C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 140-321 FROM N.A.
RC   STRAIN=968 H90;
RA   Ding D.;
RT   "Generation and analysis of GFP-gene fusion library of fission
RT   yeast.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO C.ELEGANS R11A8.2.
DR   EMBL; AL022070; CAA17782.1; -.
DR   EMBL; AB027944; BAA87248.1; -.
DR   InterPro; IPR000467; G_patch.
DR   SMART; SM00443; G-patch; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   381 AA;  44214 MW;  E1542538B667549F CRC64;

  Query Match             10.5%;  Score 85;  DB 3;  Length 381;
  Best Local Similarity   26.4%;  Pred. No. 2.1;
  Matches   39;  Conservative   23;  Mismatches   54;  Indels   32;  Gaps    7;

Qy       3 GKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAV 62
           |:| || :   ::| :  |:  | :|:  ::|: |   |  :|:|
Db     208 GQLSSKDAF--DVNQRPTFLGMGAKPVDSELTELDIWKNPKKTMF--------------- 250

Qy      63 TISVK-CEKISXLSCENKIISF-KEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
           : ||  |  | |: :|:   . |: |  ||:  | |  :| :||    || :  |||
Db    251 -LPVKPLESNSALNSQNEHTEVQKKSNSIDNL--TPSSELFRKRS---RDNNLSRESS-- 302

Qy    121 EGYFLACEKERDLFKLILKKEDELGDRS 148
                |  |       | |   ||:
Db    303 -----VSSKHLDYNSRNYNKRDRDPDRT 325


RESULT 15
O74316
ID   O74316      PRELIMINARY;      PRT;   263 AA.
AC   O74316;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 30.3 kDa protein.
GN   SPBC15D4.11C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Gaillardin C.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL031349; CAA20486.2; -.
DR   InterPro; IPR003428; MAM33.
DR   Pfam; PF02330; MAM33; 1.
SQ   SEQUENCE   263 AA;  30254 MW;  F5673E959584C99B CRC64;

  Query Match             10.1%;  Score 82;  DB 3;  Length 263;
  Best Local Similarity   21.7%;  Pred. No. 2.8;
  Matches   35;  Conservative   33;  Mismatches   65;  Indels   28;  Gaps    5;

Qy       4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVT 63
           ||:|:|  :: : |: |      : |   :   |       ::  ||  |::    : ||
Db      47 KLDSELGYVKQVLDETLPKKGYEKALHSFIIHED------PSLNYISALKETAKERIRVT 100

Qy      64 ISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGH-------------- 109
           : |   : | :  : | |:    |  :|  :|  :::||| |:| :
Db     101 VPVYSSRKSYV--QTKPITHSAEN--ENGNETSDELVFFQHSIPAYVQLTNNHGTILCAL 156

Qy     110 ---DNKMQFESSSYEGYFLACEKERDLFKLILKKEDELGDR 147
               : |:| |::    :     || :|||:|  :   |
Db     157 ILCKGMLHFDSISFQSPQNSQAFSSDL-RLILQKSQKYTGR 196


Search completed: April  4, 2003, 11:01:23
Job time : 88 secs
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